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Maximum DB seq length: 2000000000
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution:
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1: /cgn2_6/ptodata/2/

2: /cgn2_6/ptodata/2/

3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-790-912-4
PCT-US93-07261-11
PCT-US93-07261-16
US-08-596-291-3
US-08-196-291-3
US-08-296-791-3
US-08-296-791-3
US-08-296-791-19
US-08-296-791-19
US-08-663-112-2
52331168-2
         US-08-296-791-6
PCT-US95-10661A-6
US-08-480-604A-10
US-08-915-136-10
US-08-915-136-10
US-08-915-136-10
US-08-296-791-5
PCT-US95-10661A-5
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US-08-480-5-496A-21
US-08-480-604A-30
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US-08-915-136-30
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470.363 Million cell updates/sec
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Sequence 18, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 16, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
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Sequence 2, Appli
Sequence 2, Appli
Patent No. 5231168
Sequence 6, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 10, Appl
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             Sequence
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22 SYOLGKHHMGSATKD-NQIAYIDDSKGKAKAPKTNKTMDQISAEEGISAEQIVVKITDQG 80

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; Sequence 66, Applicat
; Patent No. 6159469
; GENERAL INFORMATION:
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US-08-961-083-66
                                                                MOLECULE TYPE: protein US-08-961-083-66
                                                                                                                  INFORMATION FOR SEQ ID NO: 666.
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amin
 Query Match
Best Local Similarity
Matches 285; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi et.
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                     COMPUTER: HP Vectra 486
OPERATING SYSTEM: MSDO:
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                          TOPOLOGY: li
                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                      NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
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23.6%; Score 1032; DB 4; Length 763; ilarity 33.6%; Pred. No. 8e-76; Conservative 101; Mismatches 249; Indels 21:
                                                                                           linear
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                                                                                                     single
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PCT-US94-09943-2

US-08-701-380-2

US-09-032-365A-13

US-07-854-596B-40

US-08-488-940-2

US-09-040-843-4

US-09-040-843-4

US-08-613-009A-10

US-08-613-009A-9

US-08-488-940-1

US-08-488-940-18

US-08-67-941-25

US-08-867-941-25
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      Indels 212;
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Sequence 2, Appli
Sequence 2, Appli
Sequence 13, Appl
Sequence 40, Appli
Sequence 46, Appli
Sequence 4, Appli
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Sequence 2, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 17, Appli
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Sequence 17, Appli
Sequence 18, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 25, Appli
Sequence 25, Appli
        Gaps
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US-08-961-083-56
                                                                                                                                                                                                                     Sequence 56, Application US/08961083 Patent No. 6159469 GENERAL INFORMATION:
                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                               APPLICANT: Choi et. al.

**TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

**NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                   684 KNGQADT 690
                                                                                                                                                                                                                                                                                                                                                                                                                              808 KNGELVT 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                          633 FEWFDEGLYEAPKGYTLEDLLATY------KYYVEHPNERPHSDNGFGNASDHVQ-RN 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573 STDHQDSGNTEAKGAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIK 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    677 DVLAKETEVWKDGSFSIPRADGSSLRTINKSDLSQAEWQQAQELLAKKNAGDATDTDKPK 736
    COUNTRY:
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                                           STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 V-----GDGY------VFEENGVSRYIPAKDLSAETAAGIDSKLAKQESL--S
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                                                                          ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 RYRSNHWVPD---SRPEQPSPQSTPEPSPSPQPAPNPQPAPSNPIDEK----LVKEAVRK 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDIWSKPGHEESGSVIPNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFATPDGYIFDPR 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPRLAVDVSSLPMHAGNATYDTGSSFVIPHIDHIHVVPYSWLTRDQIATIKYVMQHPEVR 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELAD---- 376
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Ş В Ş 밁 Ş 밁 QΥ Б Ş В δõ 밁 Ş 밁 Š а δÃ 밁 Ş В δÃ 망 Qy 밁 ρy Вb Ş B

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; MOLECULE TYPE: protein US-08-961-083-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
512 EDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQA 571
                                              421 ------YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVAN 468
                                                                                              452 KALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYT
                                                                                                                                                                                             392 KGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAH
                                                                                                                                                                                                                                           392 -----IKAY-----
                                                                                                                                                                                                                                                                                            332 PLRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEE 391
                                                                                                                                                                                                                                                                                                                                                                                          272 KQLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARII 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                         377 --RYLAGQTEDD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                        319 DQLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELAD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 QNSDNTSRTNW-VPSVS-NPGTTNTNTSN-----NSNTNSQASQSND-----IDSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 IFSPTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRG--ARPSDYRP 258
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 KDAAHADNVRTKEEINRQKQEHSQH-REGG-----TPRNDGAVALARSQGRYTTDDGY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 KPGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGY 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 YVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 YVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYRFKOSDVINEILDGYVIKVNGNYYYYL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 SYQLGKHHMGSATKDNQIAYIDDSKGKAKAPKT-NKTMDQISAEEGISAEQIVVKITDQG 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SYELGLYQARTYKENNRYSYID----GKQATQKTENLTPDEVSKREGINAEQIVIKITDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brookes, A Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/961,083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLS---GRGNLSNSRTYRR 226
                                                                                                                                                              --GKGLD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 100; Mismatches 214; Indels 348; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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; MOLECULE TYPE: US-08-961-083-182
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Query Match 19.2
Best Local Similarity 39.9
Matches 178; Conservative
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                                                                                                                                                                                                                                           TELEFAX: (301) 309-85
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 36,373
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAY: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   756 GLRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEK 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  679 LAKETFVWKDGSFSIPRADGSSLRTINKSDLSQAEWQQAQELLAKKN----AGDATDT-- 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681 GW------GNASEHVLGKKDHSEDPNKNFKADEEPVEETPAE-----PE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 PKDGKDYFYARDQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAGN 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572 YTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLV------RLPYMV 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               619 IWSKPGHEESGSVIPNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRDV 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 WVKAKG------QADELAAALDQEQGKEK-PLFDTKKVSRKVTKDGKVGYMM 513
                                                                                                                                         LENGTH: 447 amino aci
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/961,083 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.5
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS ve.
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                              309-8512
19.2%; Score 839; DB 4
39.9%; Pred. No. 2e-60;
tive 65; Mismatches 1
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                                     DB 4; Length 447;
    119;
    Indels
  84;
  Gaps
  10;
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                       TELEX: 831-494
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                             NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-220
TELEPHONE: (215) 567-201
                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/026,939
FILING DATE: 23-SEP-196
ATTORNEY/AGENT INFORMATION:
NAME: 1 TOWN WESTERNATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Weiser, Jeffrey N. APPLICANT: Plaut, Andrew G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 IFNPKDIVEETATAYIVRHGDHFHYI 379
                                            TELEPHONE: (215) 567-2991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 PSAQRYSESDGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIA-RMVPISGT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 NNTQSVAKGSTSKPAN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 TDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDYRPTPAPAP 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 HADNVRTKDEINRQKQEHVKD-NEKVNSNVA------
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 29-JAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 LGKHHMGSATKDNQIAYIDDSKGKAKAPKTNKTMDQISAEEGISAEQIVVKITDQGYVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LNQHRSQENKDNNRVSYVDGSQSSQKS--ENLTPDQVSQKEGIQAEQIVIKITDQGYVTS
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708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 E----QVTPLPEYTGTQAGAVVSPEQVAPLPEYTGTQSGAIVEPAQVTPLPEYTGVQSGA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 GSKRKNIR-----TKQQIAEQVAKGTKEAKEKGL-----
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                                                                                                                                                                                                            592 -VVPYSWLTRDQIATIKYVMQHPEVRPDIWSKPGHEESGSVIPNVTPLDKRAGMPN--WQ 648
                                                                                                                                                                                                                                                               831 INALVDKSKATITISS---NADSTNQTVGGLAGLVEKDALISNSYAEGNINNVKRFGSVA 887
                                                                                                                                                                                                                                                                                                                556 I----EPRLAVDVSSLPMHAGNATYDTG-----
                                                                                                                                                                                                                                                                                                                                                                 771 TRINNYHYDGYLAGERGIGGLYWKADNSKISNSSFKGRIVNSYETKAPYNIGGLYGQLTG 830
                                                                                                                                                                                                                                                                                                                                                                                                                 530 TQIAFAEQELMLKDKK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                               724 KNYAI---YNLKKPLFDTLSAATVENLTLKDVNISGKTDIGAL------ANEANNA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 DAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAK------GQADE 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 QLSPLEMELADRYLAGQTEDDDSGSDHSKPSDKEVTH-TFLGHRIKAYGKGLDGKPYDTS 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 GKYKQHVSLDAIPSNQENYFVKVKSSKFKDVFLPISSIVDSTKDGQPV-----YKITASA 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 LKYR-HVEEDGL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 HGNHYHYIPKKD------LSPSELAAAQAYWSQKQGRGARPSDYRPTP-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 PLPEYTGVQSGAIVEPEQVASLPE:----YSGTLSGAIVEPEQIEPEIGGVQSGAIVEP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 HLSK------EEVAAVNEAKROGRYT-TDDGYIFSPTDIIDDLG----DAYLVP 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 GRKIEVVRIFTVDNAEVSREVLSTKIEEATPKIVEKGTKKLEAPSEKPVTSNLVQPEQVA
                                                                     946 VTLEKDEVVTKESLEER-----GTILDVSQIASKKSEI---NSLSAPKVETLLTSTNKES 997
                                                                                                              649 I-IHSAEEVQKALAEGRFATPDGYIFDPRDVLAKETFVWKDGSFSIPRADGSSLRTINKS 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 GHQPD-----NGGYHPAPPRPND----ASQNKHQRDE-FKGKTFKELLD-QLHRL-D 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 DNQIAYIDDSKGKAKAPK----TNKTMD-QISAEE-GISAEQIVVKITDQGYVTSHGDHY 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------PQDEVLSGR--VAKPELLYKETSIETEIAYGEQIQENPDLAEGTVRVKQEGKP 295
                 DLSQAEWQQAQELLAKKNA------GDATDTDK---PKEKQQADKSNENQQ 749
                                                                                                                                                                 GVAGYLW-DRDS-SEERHAGRLHNVLSDINVMNGNAISGYHYRGMRITDSYSNKDNRVYK 945
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; Sequence 11, Application PC/TUS9307261
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.3%; Score 142.5; DB 5; Best Local Similarity 20.0%; Pred. No. 0.01; Matches 174; Conservative 120; Mismatches 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07940-1000
COMPUTER READABLE FORM:
MEDIM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/927,531
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 1993080 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1588 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                         136 -YYVYLKPGSKRKNIR----TKQQIAEQVAKGTKEAKEK------
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STATE: New Je
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                                                                                                                               KKIVPKKPESVEKDLKEMELKEKEFIKQHLKDYEERKEKRRNWILRSLRRDKLREIEQLE 166
                                                                                                                                                                                                                                                                                                                                                KHHMGSATKDNQIAYIDDSKGKAKAPKTN-----KTMDQISAEEGISAEQIVVKITDQGY 81
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    GDAY--LVP---HGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDYRPTPAPAPGR 266
                                              KLNAQLESAINELKERRASRRPMMVKMQRGMKDEVDEWIKKYDDEQAEKNGTKDEEIKDK 226
                                                                                      HLSKEEVAAVNEAK -----
                                                                                                                                                                                                                 KEKE------NKETLKKKELENQKEKEEKNKIKDNNDEALKNKGNDKDD 106
                                                                                                                                                                                                                                                         VTSHGDHYHFYNGKVPYDAIISEELLMTDPNYRFKQSDVINEILDG--YVIKVNGN----
                                                                                                                                                                                                                                                                                                        KEALKQKTEKNEKARNALKEKKLKEQKKNDAQKAKDLTKKESQDSSSEKSLKEKVNGEAL 63
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GENERAL INFORMATION:
GENERAL INFORMATION:
FEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. C. Blasdale
APPLICATION NUMBER: US 07/927
FILING DATE: 07-AUG-1992
ATTORNEY_AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DOC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/927,531
                                                                                                                                                                                                       SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649 P-HENLEEY--NETDLAKGKEVTNKPHESVDEYDQSELAKGKDITNKPHESVDEY---DQ
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                                                                                                                                                                APPLICATION NUMBER: POFILING DATE: 19930805
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; ORIGINAL SOURCE:
; ORGANISM: Plasmodium
; STRAIN: Malayan Camp
PCT-US93-07261-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
                                               677 DVLAKETFVWKDGSFSIPRADGSSLRTINKSDLSQAEWQQAQELL--AKKNAGDATDTDK 734
                                                                                                                                                                                                                                                   575 TYDTGSSFVIPHIDHIHVVPYSWLTRDQIATIKYVMQHPEVRPD------IWSK
                                                                                                                                                                                                                                                                                                     552 SREYQLDNEGPSTLKEYDQTELAKGKDITNKPHESVDEYDQTELAKGKDITNKP-HESVD 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 RKAPIPDYTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLDQLHRLDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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TELAK - - - -
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                                                                                                 P-HENLEEY--NETDLAKGKEVTNKPHESVDEYDQSELAKGKDITNKPHESVDEY---DQ 702
                                                                                                                                                 PGHEESGSVIPNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFAT-----PDGYIFDPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -YYVYLKPGSKRKNIR----TKQQIAEQVAKGTKEAKEK------GLAQVA 175
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                                                                                                                                                                                                 ---QSELAKGKDITNKPHESVDEYDQTELAKGKEVTNK
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US-08-596-291-3
                                                                                                                                                                                                                                                                                                                                          Query Match 3.0%; Score 133; DB 2; Length 2465; Best Local Similarity 19.9%; Pred. No. 0.12; Matches 176; Conservative 114; Mismatches 322; Indels 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617/720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 3:
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APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCT
TITLE OF INVENTION: TYROSINE PHOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: LO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DC-DOS/MS-DOS
COMPUTER: DC-DOS/MS-DOS
                                                                                                                                                               1477
                                                                                                                                                                                                                                                   1422 GQVVHLLLEK.-GQSPTSKEHVPVTPQCTLSDQNA---QGQGPEKVKKTTQVKDYSFVTE 1476
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FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino aci
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                                                                    1535 L----KVNG----ASLKGLSQQEVISALRGTAPEVFLLLCRPPPGVLPEIDTALLTPLQS 1586
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155 IAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAK-----ROGRYTT-----DDGYIFS 203
                                                                                                                125 LDGYVIKVNGNYYVYLKPGSKRKNIRT-----
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STREET: 600 ACCITY: BOSTON
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TELEFAX: 617/720-2441
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ZIP: 02210
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                                                                                                                                                          ENTFEVKLFKNSSGLGFSFSRED--NLIPEQINASIVRVKKLFAGQPAAESGKIDVGDVI 1534
                                                                                                                                                                                                         EGISAEQIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYRFKQSDVINEI 124
                                                                                                                                                                                                                                                                                                GSVAAILLATHIGSYQLGKHHM----GSATKDNQIAYIDDSKGKAKAPKTNKTMD-QISAE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2465 amino acids
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N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/596,291
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                                                                                                                                                                                                                                                                                                                                          Indels 272; Gaps
                                                                                                                -----KQQ 154
                                                                                                                                                                                                                                                                                                                                               44;
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	OMPUTER READABLE FORM: MEDIUM TYPE: Flopy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 URRENT APPLICATION DATA:	ი ი	
PROTEIN	2 ZO EESZZZ	CONU	
	CCEEKVKSESLIQKE 104-3 104-3 3, Application 1, 6066472 INFORMATION: ANT: GANEX; ANT: SAREX; ANT: CLAESSON	ESUL S-09 Seq Pat GE	
	746ENQQPSEASKEEEKESDDFIDSLPDYGLDRATLED 780	0у 7	
745 2104	713 EWQQAQELLAKKN-AGDATDTDKPKEKQQADKSN : :: :	Qy 7 Db 20	
712 2045	656 VQK-ALAEGRFATPDGYIFDPRDVLAKETFVWKDGSFSIPRADGSSLRTINKSDLSQA :::	Qy 6 Db 19	
655 1993	597 WLTRDQIATIKYVMQHPEVRPDIWSKPGHEESGSVI-PNVTPLDKRAGMPNWQIIHSAEE	Qy 5 Db 19	
596 1953	540 MLKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPHIDHIHVVPYS	Qy 5 Db 19	
539 1905	480 AAALDQEQGKEKPLFDTKKVSRKVTKDGKVGYMMPKDGKDYFYARDQLDLTQIAFAEQEL	Qy 4 Db 18	
479 1873	420 PYDTSDAYVESKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADEL	Qy 4 Db 18	
419 1848	374 LADRYLAGQTEDDDSGSDHSKPSDKEVTHTFLGHRIKAYGKGLDGK	Qy 3 Db 17	
373 1788	317 LLDQLHRLDLKYRHVEEDGLIFE-PTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEME	Qy 3 Db 17	
316 1745	257 RPTPAPAPGRRKAPIPDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKE : : : : : : : : : :	Qy 2 Db 17	
256 1703	204 PTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDY 	Qy 2 Db 16	
1646	587 PAQVLPNSSKDSSQPSCVEQSTSSDENEMSDKSKKQCKSPSRRDSYSDSSGSGEDDLVTA	Db 15	

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                                                 1874 GFSL---CGGHDSLYQVVYIS--
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FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWAAD R.
REGISTRATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                                                                           317 LLDQLHRLDLKYRHVEEDGLIFE-PTQVIKSN--AFGYVVPHGDHYHIIPRSQLSPLEME 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: LO TELECOMMUNICATION INFORMATION: 517-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 IAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAK-----RQGRYTT-----DDGYIFS 203
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-720-2441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                     PYDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADEL 479
                                                                                                                                                                                                                                                         LADRYLAGQTEDDDSGSDHSKPSDK-----EVTHTFLGHRIKAYGKG----LDGK 419
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                                                                                   AAALDQEQGKEKPLFDTKKVSRKVTKDGKVGYMMPKDGKDYFYARDQLDLTQIAFAEQEL 539
                                                                                                                                   PRITQNTNVASFATGH------
                                                                                                                                                                                                                RIGCYVHDVIQDPAKSDGRLKPGDRLIKVNDTDVTNMTHTDAVNLLRAASKTVRLVIGRV 1848
                                                                                                                                                                                                                                                                                                      NWTPL-KNDLE-NHLEDFELEVELLITLIKSEKASLGFTVTKGN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTDIIDDLGDAYL------VPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDY 256
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NUMBER: US 08/115,573
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Sequence 3, Application US/08296791
Patent NO. 6245337
GENERAL INFORMATION:
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                                                                                                                                                                           Query Match 3.0%; Score 131.5; DB 4; Length 1541; Best Local Similarity 17.5%; Pred. No. 0.078; Matches 153; Conservative 111; Mismatches 294; Indels 315;
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: St. Geme III, Jo
APPLICANT: Falkow, Stanley
TITLE OF INVENTION: Haemoph
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1541 amino acids
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1994 INEISYPKGKCST---YQIKGSPNLTLPKESYIQEDDIY-----DDSQEAEVIQSLLDVV 2045
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522 LDLNGNSLTFDHIRNIDDGARLVNHNMTNASNITITGESLITDPNTITPYNIDAPDEDNP
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                                                                                    462 DNKGSLKVGDGTVILKQQTNGSGQHAFASVGIVSGRSTLVLNDDKQVDPNSIYFGFRGGR 521
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CITY: San Francisco
CITY: 7-14 fornia
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                                                                                                                                        44 DSKGKAKA----
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                              ------VPYDAI-----
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                                            ------ISEELLMTDPN----YRFKQSDVIN- 122
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                                   COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1137 ETVQPQAEPAREN-DPTVNIKEPQSQTNTTADT 1168
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1041 AENSKQESKTVEKNEQDATETTAQ-NREVAKEAKSNVKANTQTNEVAQSG--SETKETQT 1097
                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Washington University, et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                515 KDGKDYFYARDQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPR-----L 560
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                                                                                                                                                                                       STATE:
                                                                                                                                                                                                           STREET: 4
CITY: San
                                                                                                                                                                                                                                                             ADDRESSEE:
SOFTWARE:
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                                                                                                                                                                                       California
                                                                                                                                                                                                                                    E: Flehr, Hohbach, Test, Albritton & Herbert 4 Embarcadero Center, Suite 3400
                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                Francisco
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER: US 08/296,791
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LENGTH: 1541 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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561 AVDVSSLEMHAGNATYDTGSSFVIPHIDHIHVVPYSWLTRDQIATIKYVMQHPEVRPDIW 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
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                                                                                                                           TDLSNKQGDKVVVTKSATGNFTLQVADKTGEPNHNELTLFDASKAQRDHLNVSLVG---- 959
                                                                                                                                                                                                                                                                                                       KANLFGTIQSRGNSQVRLTENSHWHLTGNSDVHQLDLA------NGHIHLNS 876
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                                                                                                                                                                       GELEQYELDEVANWVKAKGQAD-ELAAALDQEQGKEKPLFDTKKVSRKVTKDGKVGYMMP 514
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                                                                                  KDGKDYFYARDQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPR---
                                           ------NTVDLGAWKYKLRNV-----NGRYDLYNPEVEKRNQTVDTTNITTPNNI 1003
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Query Match 2.9%; Score 128.5; DB 2; Length 1076; Best Local Similarity 20.1%; Pred. No. 0.08; Matches 141; Conservative 87; Mismatches 244; Indels 231; Gaps 40; 3 KTYGYIGSVAAILLATHIGSYQLGKHHMGSATKDNQIAYIDDSKGK 48	MION MION MION MION MION MICH MIN	11 11 12. Application US/08867941 nt No. 5977337 ERAL INFORMATION: PPLICANT: Loosmore, Sheena M PPLICANT: Wang, Quijun PPLICANT: Wang, Quijun PPLICANT: Klein, Michel H PPLICANT: Klein, Michel H ITLE OF INVENTION. LACTOFERRIN RECEPT WHER OF SEQUENCES: 67 ORRESPONDENCE ADDRESS: ADDRESSE: Sim & MCBUrney STREET: 6th Floor, 330 University Av CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: MSG 1R7 OMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS	1
	URES POS	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
ER READIM TYPOTTER: ATING ATING WARE: WARE	RESULT 12 US-09-074-658-19 US-09-074-658-19 Sequence 19, Application US/09074658 Patent No. 6184371 GENERAL INFORMATION: APPLICANT: LOOSMOTE, Sheena M APPLICANT: LOUIJUN WANG APPLICANT: Yang, Yan-Ping APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel H TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA NUMBER OF SEQUENCES: 78 CORRESPONDENCE ADDRESS: ADDRESSEE: Sim & MCBurney STREET: 6th Floor, 330 University Avenue CITY: Toronto STATE: Ontario COUNTRY: Canada 21P: M5G 1R7	ELLDQLHRLD:	263 VATTDPNNRTFLIANECANGNYEACAAGGQTKLQAKPTNVRDKVNVK 309 157 EQVAKGTKEAKEKGLAQVAHLS-KEEVAAVNEAKRQGRYTTDDGYIFSPTDII 208 158 EURICH STEELEN S

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                                                                                          Sequence 2, Application US/08663112 Patent No. 5849503 GENERAL INFORMATION:
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Best Local
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 1076 amino acids
APPLICANT: WAGATSUMA, MASAKO
APPLICANT: KURITA, NO. 58495031kO
TITLE OF INVENTION: MUTANT PROTEINS
TITLE OF INVENTION: TOPOISOMERASE I
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                                                                                                                                                                                                                                                                                                                                                                                    512 MMPKD-------GKDYFYARDQLDLTQIAFAEQELMLKDKKHYRYDIV 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461 YELDEVANWVKAKGQADEL--AAALDQ--EQGKEKPLEDTKKVSR-----KVTKDGKVGY 511
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRKAPIPDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEF------KGKTFK 315
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                           OF HUMAN DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-NOV-1996
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Einaudi, Carolyn P.
REGISTRATION NUMBER: 32,220
REFERENCE_POCKET NUMBER: 0666
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 765 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                             542 KDKKHYRYDIVDTGIEPR----LAVDVSSLPMHAGN-----ATYDTGS--SFVIPHID--
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KIRNQYREDWKSKEMKVRQRAVALYFIDKLALRAGNEKEEGETADTVGCCSLRVEHINLH 515
                                                                                          HDNKVTWLVSWTENIQGSIKYIMLNPSSRIKGEKDWQKYETAR------RLKKCVD 455
                                                                                                                                                                                                                               TAKHGDHFHYIGFGELEQYELDE - - VANWVKAKGQADELAAALDQEQGKEKPLFDTKKV -
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                                                                                                                                       -SRKVT-----KDGKVGYMM------PKDGKDYFYARDQLDLTQIAFAEQELML
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20.1%; Pred. No. 0.063;
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FILING DATE: 18-SEP-1989
:SEQ ID NO:2:
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VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: MALARIA ANTIGEN NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548 FKNLQLFMENKQ------PEDDLFDRLNTGILNKHLQDLMEG-----LTAKVF 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644 MPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRD~-VLAKETFVWKDGSFSIPRADGSSL 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 YIDDSKGKAKAPKTNKTMDQISAEEG------ISAEQIVVKITDQGYVTSHGDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 783
HEIVEV----EEILPEDDKNEKVEHEIVE--VEEILPEDKNEKGQHE----
                                                                                                                                                                                     KGLDGKPYDTSDAYVFSK-----ESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEV 466
                                                                                                                                                                                                                             DEFEDVHTEQLD------LDHKTVDPEIVEVEEIPSELHENEVAH------
                                                                                                                                                                                                                                                              DHYHIIPRSQLSPLEMELADRYLAGQTEDDDSGSDHSKPS---DKEVTHTFLGHRIKAYG
                                                                                                                                                                                                                                                                                                      VPSEENKHASVDPEVKE-KENVSEV------VEEKQNSQESVEEIPVNE-----
                                                                                                                                                                                                                                                                                                                                                                               SNNEPSEKKDGPVPSKPFEEIEKVDVQPKIVDLQIIEPNFVDSQPNPQEPVEPSFVKIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDSELSENELVESEKSVSEPAEHVEIVSEKSVSEPAEHVEIVSEKSTSEPAEHVESVSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIDDLGDAYLVPH-----GNHYHYIPKKDLS-PSE-----LAAAQAYWSQKQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEAHQEEIVPEQ----NDEESGESGLVD------NE---EGDFEEPNHEEFEPDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y--HFYNGKVPYDAIISEELLMTDPNYRFKQSDVINEILDGYVIKVNGNYYVYLKPGSKR 146
                                   LDLTQIAFAEQELMLKDKKHYR--YDIVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVI 584
                                                                                                              ANWVKAKGQADELAAALDQEQGKEKPLFDTKKVSRKVTKDGKVGYMMPKDGKDYFYARDQ 526
                                                                                                                                                                                                                                                                                                                                         ----QNKHQRDEFKGKTFKELLDQLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHG
                                                                                                                                                                                                                                                                                                                                                                                                                  RGARPSDYRPTPAPAPGRRKAPIPDVTPN--PGQGHQPDNGGYHPAPPRPNDAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGYIFSPTD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSSEVSNSELNENEFVESDKSVTEP---AEHEEVVSE-----ESNPEPAENEESSI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVESEKSEHEAAEN----EESSLEEGHHEEIVPEQNNEESGESKLVDNDEGGFEEAHHEN 57
                                                                                                                                                  -----PEIVEIEEVFPEPNQNNEFQEINEDDKSA-----HI------QHEIVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PELDGQEYVVEFDFLGKD---SIRYY-----
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                                                                           -----EEILPEDDKNEKVEHEIVEVEEI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.9%; Score 127; DB 6; Length 783; nilarity 17.9%; Pred. No. 0.065; Conservative 147; Mismatches 309; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/07/409,658
                                                                           Indels 246;
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; TOPOLOGY:
US-08-296-791-6
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US-08-296-791-6
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                                                                                                                                  Matches
                                                                                                                                                   Best Local
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: St. Geme III, JC
APPLICANT: Falkow, Stanley
TITLE OF INVENTION: Haemoph
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION: NAME: Trecartin, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                     101
                                                           487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            585 PHIDHIHVVPYSWLTRDQIATIKY-VMQHPEVRPDIWSKPGHEESGSVIPNVTPLDKRAG 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/296,791 FILING DATE: 25-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Trecartin, Richard F REGISTRATION NUMBER: 31,80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                     KQKADANNKV--QAFSQVGIVSGRSTLVLNDDKQVDPNSIYFGFRGGRLDLNGNSLTFDH 544
                                                                                          KAKAPKTNKTMDQISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGK------VPYDA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEEKESDDFID--SLPDYGLDRATLEDHINQLAQKANIDPKYLIFQPEGVQFYNKNGELV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEVEEI-----LPEDKNEKVEHEIVEVEEILPEDKNEKGQHEIVEV-EEILPEDK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDKNEKVQHEIVEVEEILPEDKNEKVQHEIVEVEEILPEIVEIEEVPSQTNNNENIETIK 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPNWQIIHSAEEVQKALAEGRFATPDGYIFDPRDVLAKETFVWKDGSFSIPRADGSSLRT 703
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                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                 1848 amino acids
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                unknown
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flehr, Hohbach, Test, Albritton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1994
N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                 2.8%; Score 124; DB 16.9%; Pred. No. 0.42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus Adherence and Penetration
                                                                                                                                                                                                                                                                                                                                                                                                                                 31,801
               ---ISEELLMTDPN----YRFKQSDVINEILDGYVIKV--- 132
                                                                                                                              125;
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                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1
                                                                                                                                                                 DB 4; Length 1848;
                                                                                                                                336;
                                                                                                                                Indels 302;
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                                                                                                                              Gaps
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Db	545	TRNIDDGARVVNHNMTNTSNITITGESLTTNPNTITSYNTEAQDDDHPLRIRSI 598
P &	133 599	
Qy	168	EKGLAQVAHLSKEEVAAVNEAKROGRYTTDDGYIFSPTDIIDDLGDAYLVP 218
Db	659	MNGFNGYFGEEETKATQNGKLNVTFNGKSDQNRFLLTGGTNLNGDLN 705
Qy	219	HGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDYRPTPAPAPGRRKAPIPDVTPNP 278
망	706	VEKGTLFLSG719
Qy	279	GQGHQPDNGGYHPAPPRPNDASQNK-HQRDEFKGKTFKELLDQLHRLDLKYRHVEEDGLI 337
Db	720	HARDIAGISSTKKDPHFTENNEVVVEDDWINRNFK754
νQ	338	FEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELADRYLAGQTEDDDSGSDH 392
В	755	-ATTMNVTGNASLYSGRNVANITSNITASNNAQVHIGYKTGDTVCVRSDYTGYVTCH 810
Qy	393	SKPSDKEVTHTELGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGDHFHY 452
ρb	811	NSNLSEKALNSENPTNLRGNVNLTENASFTLGKANLFGTIQSIGTSQVNLKENSHWHL 868
Qγ	453	IGFGELEQYELDEVANWYKAKGQADELAAALDQEQGKEKPLFDTKKVSRKVTKDGKYGYM 512
Дb	869	TGNSNVNQLNLTNGHIHLNAQNDANKVTTYNTLTVNS 905
Qy	513	MPKDGKDYFYARDQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPRLAV 562
Вb	906	LSGNGSFYYWVDFTNNKSNKVVVNKSATGNFTLQVADKTGEPNHNELTLFDASNATR 962
Qy	563	DVSSLPMHAGNATYDTGSSFVIPHIDHIHVVPYSWLTRDQIATIKYVMQHPEVRPDIWSK 622
B	963	NNLEVTLANGSVDRGAWKYKLRNVNGRYDLYN- 994
Qy	623	PGHEESGSVIPNVTPLDKRAGMPNWQIHSAEEVQKALAEGRFAT 667
Вb	995	PEVEKRNOTVDTTNITTPNDIQADAPSAQSNNEEIARVETPVPPPAPATESAIASEQPET 1054
Qy	668	PDGYIFDPRDVLAKETFVWKDGSFSIPRADGSSLRTINKSDLSQAEWQQAQE 719
дь	1055	RPAETAQPAMEETNTANSTETAPKSDTATQTENPNSESVPSETTEKVAENPPQENE 1110
Qy	720	LLAKKNAGDATDTDKPKEKQQADKSNENQQPSEASKEEEKESD 762
рь	1111	TVAKNEQEATEPTPQNGEVAKEDQPTVEANTQTNEATQSEGKTEETQTAE-TKSEPTESV 1169
Qy	763	DFIDSLPDYGLDRATLEDHINQLAQKANID
Дb	1170	TVSENQPEKTVSQSTEDKVVVEKEEKAKVETEETQKAPQVTSKEPPKQAEPAPEEVP-TD 1228
Qy	808	KNGELVTYDIKTLQQINP 825
В	1229	TNAEEAQALQQTQP 1242

Search completed: December 3, 2001, 07:16:03 Job time: 132 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
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6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                        Query
                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          December 3, 2001, 07:16:03; Search time 39.47 Seconds (without alignments) 451.548 Million cell updates/sec
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Copyright (c) 1993 - 2000 Comp
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       708
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 PCT-US95-10509-2
US-08-961-083-56
US-08-961-083-66
US-08-961-083-66
US-09-131-648-2
US-09-1353-585-3
US-09-180-439-3
US-09-180-439-6
US-09-180-439-6
US-08-190-802A-50
US-08-477-346-50
US-08-473-553A-6
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US-08-619-160-2
US-08-619-916-2
US-08-619-916-2
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Sequence 2, Appli sequence 56, Appl sequence 56, Appli sequence 2, Appli sequence 3, Appli sequence 3, Appli sequence 3, Appli sequence 4, Appli sequence 4, Appli sequence 50, Appli sequence 50, Appli sequence 49, Appli sequence 49, Appli sequence 6, Appli sequence 2, Appli sequence 3, Appli sequence 5, Appli
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ILKTVLGKTNVTDTVSQTDLDQVTTLQADRLG---IKSIDGLEYLNNLTQINFSNNQLTD VIKLDLGSRK--DPLQRKGLSLLPNLETLGIGFTPIKDISPVLQFKKLKQLLMTKTGVTD 456

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399 N

32 144 3.5 220 1 US-08-107-755A-11 Sequence 11, Appl 33 144 3.5 220 2 US-08-544-332-11 Sequence 11, Appl
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                                                                                                Query Match
Best Local Similarity
                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acid
                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 YRFLDNMPQLEGIDISQNNLKDISFLSKYKNLTLVAAADNGIEDIRPLGQLPNLKFLVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 SNTISDISALSGLTNLQQLSF-GNQVTDLKPLANLTTLERLDISSNKVSDISVLAKLTNL 177
213 STLSYSSTASDNN-----TQSVAKGSTS---KPANKSENLQSLLKEL--YDSPSAQRYS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  636 DKQGSLTFLDVTGNQLTSLEGVNNFTALDILSVSKNQLTNVNLSKPNKTVTNIDISHNNI 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 ESLIATNNQISDITPLGILTNLDELSLNGNQLKDIGTLASLTNLTDLDLANNQISNLAPL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 ETLMVNDTKVSHLDFLKNNPNLSSLSINRAQLQSLEGIEASSVIVRVEAEGNQIKSLVLK 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 SGLTKLTELKLGANQISNISPLAGLTALTNLELNENQLEDISPISNLKNLTYLTLYFNNI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 9410 Ney
CITY: Rockville
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                                        16 SQLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT----- 70
                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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9410 Key West Avenue
                                                                                                                                                                                                                                                                               447 amino acids
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                                                                                 Conservative
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                                                                                                                                                                                                                                       single
                                                                                                  5.7%; Score 233; DB 4; Length 447; 30.1%; Pred. No. 4.1e-10;
                                                                                                                                                                                                                                                                                                                                                             309-8504
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                                                                                 36; Mismatches
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                                                                                 96;
                                                                                 Indels 42; Gaps
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                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-961-083-56
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                                                                                                                                                                                   Query Match 5.5%; Score 223; DB 4; Best Local Similarity 19.5%; Pred. No. 5.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                     Matches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIVAEDALGYTVRHDDHFHYIL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 VMSHGDHNH 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 KSSLSGQTQAQAKQVATRLPQTSSLVSTATANGIPGLHFPTSDGFQFNGQGIVGVTKDSI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 AKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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58
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/961,083
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                                      90 IVVDHDGHSHFIFYADLKGSPFEYLIPKGASLAKPAVAQRAASQGTSKVADPHHHYEFNP 149
                                                                                                                           30 TYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPTDDGFILTKDSKILSKTDQG 89
                                                                                1 SYELGLYQARTVKENNRVSYIDGKQATQKT-ENLTPDEVSKREG--INAEQIVIKITDQG
YVTSHGDHYHY-----YNGKVPYDAIISEELL---
                                                                                                                                                                                                                                                                                                                                                                  amino acid
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9410 Key West Avenue
                                                                                                                                                                     Conservative 116; Mismatches 279;
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                                                                                                                                                                                                              DB 4; Length 796;
                                                                                                                                                                        Indels 300;
  --MKDP--NYKLKD 94
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; Sequence 66, Application US/08961083
; Patent No. 6159469
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COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
MEDIUM TYPE: HP Vectra 486/33
MEDIUM TYPE: MSDOS Version 6.2
                                                                                                                                                                                                                                                                       APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592 TGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYK 651
                                                                                                                                                                  STREET: 9410 Key
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --VFEEKGISRYVFAKDLP-----SETVKNLESKLSKQESVSHTLTAKKEN----VA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSPGPQP---APNLKIDSNS-----SLVSQLVRKVGEGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDPNMMKEWLATVIKLDLGSRKDPLQRKGLSLLPNL-ETLGIGFTPIKDISPVLQFKKLK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERIARIIPLRYRSNHWVPDSRP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLLKQLYKLPLSQRHVESDGLVFDPAQI----TSRTARGVAVPHGDHYHFIPYSQMSELE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLSGRGNLSNSRTYRRQNSDNTSRTNW--VPSVSNPGTTNTNTSNNSNTNSQASQSNDID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALARSQG----RYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATANGIPGLHFPTSDGFQFNGQGIVGVTKDSILVDHDGHLHPISFADL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTNVNLSKPNKTVTNIDISH--NNISLADLKLNEQHIPEAIAKN---FPAVYEGSMVGNG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVTPHMGH-----SHWIGKDSLSD---KEKVAAQAYTKEKGILPPSPDADVKANP 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----EHEDE 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAEEKAAMATKAKESAQEASESHDYNHNHTYEDEEGHA-----HEHRDK----DDHDH- 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----SQIEYTEDEVRIAQLADK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KL--VD-----DLLAFLAP------ITHPERL-GKPN------
                                                                                                                                                                                                                9410 Key West Avenue
                                                                                                                                                                                                                                    Human Genome Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YTTSDGY-IFDEHDIISDEGDA 544
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Best Local Similarity
Matches 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OFFILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 VIKVNGKYYVYLKDAAHADNIRTKEEIKRQKQERSHNHNSRADNAVAAARAQG----RYT
525
                                                                                                                              517 NNKI----SDLSPLASLHQLQELHIDNNQITDLSPVSHKESLTVVDLSRNADVDLATLQA 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 HQ-----TPELSER------EKEYQEKLAYLAEKLGIDPSTIKRVETQDGKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 TDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELA-AAEAYWNGKQGSRPSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 TSDGFQFNGQGIVGVTKDSILVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEKPAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 TVRHDDHFHYILKSSLSGQTQAQAKQVATRLPQTS----SLVSTATANGIPGLHFP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                          282 QITSRTARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEQP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 SSYNANPAQPRLSENHNLTVTPTYHQNQGENISSLLRELYAKPLSERHVES-DGLIFDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 IFYADLKGSPFEYLIPKGASLAKPAVAQRAASQGTSKVADPHHHYEFNPADIVAEDALGY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
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PRDITSDEGDAYVTPHMTHSHWIKKD-SLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTE 583
                                                                                                                                                                                                                           YRFLDNMPQLEGIDISQNNLKDISFLSKYKNLTLVAAADNGIEDIRPLGQLPNLKFLVLS 516
                                                                                                                                                                                                                                                                         GYV--FEENGVSRYIPAKDLSAETAAGIDSKLAKQESLSHKLGAKKTDLPSSDREFYNKA 434
                                                                                                                                                                                                                                                                                                                                                                                                          DTLRALGFDEEVILDIVRTHDAPTPFPSNEKDPNMMKEWLATVIKLDLGSRKDPLQRKGL 416
                                           PKLETLMVNDTKV----SHLDFLKNNPNLSSLSINRAQLQSLE-GIEASSV----IVRVE
                                                                                                                                                                                   YDLLARIHQ----DLLDNKGRQVDF---
                                                                                                                                                                                                                                                                                                                    SLLPNLETLGIG-FTPIKDISPV----LQFKKLKQ-LLMTKTGV--TD-------
                                                                                      SDKVKLYXDILAFLAPIRHPERLGKPNAQITYTD-----DEIQVAKLAGKYTTEDGYIFD
                                                                                                                                                                                                                                                                                                                                                                 ------SPQSTPEPSPSPQPAPNPQP---APSNPIDEKLVKEAVRKVGD 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GLEYPHHDHAHVL---MLSDIE--IGKDIP----DPHAIEHARELEKHKVGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.0%; Score 204; DB 4; Length 763; ilarity 19.8%; Pred. No. 1.6e-07; Conservative 125; Mismatches 314; Indels 2
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                                                                                                                                                                                     ----EALDNLLERLKD-
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CURRENT FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09131648 Patent No. 6168920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
445 RATAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGT---LDING--VTPKEGGLYTCIAT 499
                                              621 RVEAE-----GNQIKSLVLKDK-----QGSLTFLDVTGNQLTSLEG-----VN 658
                                                                                              385 NIRFMEPDSLFCVDPPEFQGQNVRQVHFRDMMEICLPLIAPESFPSNLNVEAGSYVSFHC 444
                                                                                                                                                                                             325 IHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSNPIRCDCVIRWMNMNKT 384
                                                                                                                                                                                                                                                                                                                                          513 LVLSNNKISDL--SPLASLHQLQELHIDNNQ---ITDLSPVSHKESLTVVDLSRNADVDL 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 YINHNLLSTISPG-AFIGLHNLLRLHLNSNRLQMINSKWFDALPNLEILMIGENPIIRIK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426 GIGETPIKDISPYLQEKKLKQLL----MTKTGYTDYRFLDNMPQLEGIDISQN---NLK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 TPFPSNEKDPNMMKEWLATVIKLDLGSRKDP------LQRKGLSLLPNLETL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652 TSLEGV----NNFTALDILSVSKNQLTNVNLSKPNKTVTNIDISHNNISLADLKLNEQHI 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733 SPEESEEPQVETEKVEEKLREAED 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                681 QR--NKN-----GQADTNQTEKPSEEKPQTEKPEEETPREEKPQSEKPESPKPTEEPEE 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638 ---EGLYEAPKGYTLEDLLATVKYYVEHPN-ERPHS-----DNGFGNAS------DHV 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    763 GHAHEHRDKDDHDHEHEDENEAKD 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 TDFPVNLTGLDLSQNNLSSVTNINV--KKMPQLLSVYLEENKLTELPEKCLSELSNLQEL 145
                                                                                                                                                    QLQSLE-----
                                                                                                                                                                                                                                              ----ATLQAPKLETLMVNDTKVSHL--DFLKNNPNLSSLSI--------NRA 605
                                                                                                                                                                                                                                                                                               LDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPDLRKIEATNNPRLSY 324
                                                                                                                                                                                                                                                                                                                                                                                              DMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRLIKVPHVALQKVVNLKF 264
                                                                                                                                                                                                                                                                                                                                                                                                                                            DISFLSKYKNLTLVAAADN------GIEDIR------PLGQLPNLKF 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.1%; Score 168; DB 4; Length 708; 21.7%; Pred. No. 8.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 170;
                                                                                                                                               ---GIEASSVI---V 620
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US-09-353-585-2
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Sequence 2, Application US/09353585

Patent No. 6287865

Patent INFORMATION:
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    Matches 104;
                                                   Query Match
                               Best
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
                           y Match 4.1%;
Local Similarity 24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 -- SSKILKSSVKWTAFVKTENSHAAQSARIPSDVKVYNLTH 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                719 YEGSMYGNGTAEEKAAMATKAKESAQEA---SESHDYNHNH 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 NLVGADLKSV----MIKVDGSFPQDNNGSL----NIKIRDIQAN-----SVLVSWKA-
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                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/353,585

FILING DATE: 15-Jul-1999

CLASSIFICATION: C12M 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Plant pathogen resistance genes and uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dixon, Mark S
                                                                                                                                                                       STRAIN: Cf2
                                                                                                                                                                                        ORGANISM: Tomato
                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-0CT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: GB 9506658.5 FILING DATE: 31-MAR-1995
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ms Mary J Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Nixon & Vanderhye PC STREET: 8th Floor, 1100 No. 6287865th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
    Conservative
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  49; Mismatches 141;
                           Score 167; DB 4; Length 1112; Pred. No. 0.0002;
Indels 134; Gaps
20;
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Qy

396 LATVIKLDLGSRKDPLQRKG-----LSLLPNLETLGI------GFTPIKDISPVLQFKKL 444

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RESULT 7
US-09-353-585-3
; Sequence 3, Application US/09353585
; Patent No. 6287865
; Patent No. 6287865
; GENERAL INFORMATION:
Mark S
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                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                               APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 950658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MS MARY J Wilson
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
STREET: 8th Floor, 1100 No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones, David A
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance
               TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dixon, Mark S
                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLFLYENQLAS---SVPEEIGYLRSLNVLDLSENALNGSIPASFGNLNNLSRLNLVNNQL 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPASLGNLNNLSRLYLYNNQLSGSIPEEIGYLSSLTYLDLSNNSINGFIPASFGNMSNLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington
STATE: Virginia
                                                                                                                                                                                             APPLICATION NUMBER: US 08/930,277 FILING DATE: 27-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America ZIP: 22201-4714
                                                  REFERENCE/DOCKET NUMBER: 620-69
(703) 816-4100
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                                                                                                                                                                                                                                                    1/68
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6287865th Glebe
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US-09-180-439-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09180439 Patent No. 6225532
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Best Local
                                                                               CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
EARLIER APPLICATION NUMBER: GB 9619924.5
                                                                                                                                                                                                                                                                                             APPLICANT: Jones, David A APPLICANT: Jones, Jonathan DG APPLICANT: Jones, Jonathan DG TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof FILE REFERENCE: 620 - 53
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dixon, Mark S
APPLICANT: Hatzixanthis, Kostas
                      EARLIER FILING DATE: 1996-09-24 NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver.
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;; Pred. No. 0.0002;
49; Mismatches 141; Indels 13
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; ORGANISM: Lycopersicon esculentum US-09-180-439-3
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Best Local Similarity
Matches 119; Conserv
                                                                                                                             CURRENT APPLICATION NUMBER: US/09/180,439 CURRENT FILING DATE: 1998-12-06 EARLIER APPLICATION NUMBER: PCT/GB97/01249 EARLIER FILING DATE: 1997-05-08
                                                                                                                                                                                                                                                             APPLICANT: Dixon, Mark S
APPLICANT: Hatzixanthis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
                    EARLIER APPLICATION NUMBER: GB 9619924.5
EARLIER FILING DATE: 1996-09-24
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                      TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof FILE REFERENCE: 620 - 53
SOFTWARE: PatentIn Ver.
                                                                                    EARLIER APPLICATION NUMBER: GB 9 EARLIER FILING DATE: 1996-05-09
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; LENCTH: 968
; TYPE: PRT
; ORCANISM: Lycopersicon esculentum
US-09-180-439-4
            CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER FILING DATE: 1996-05-09
EARLIER FILING DATE: 1996-05-09
EARLIER FILING DATE: 1996-09-24
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09180439 Patent No. 6225532 GENERAL INFORMATION:
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Best Local Similarity
Matches 119; Conserv
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APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance
FILE REFERENCE: 620 - 53
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APPLICANT: Hatzixanthis, Kostas
SOFTWARE: PatentIn
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Pred. No. 0.00057;
8; Mismatches 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08303238
Patent No. 5654270
GENERAL INFORMATION:
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LENGTH: 799
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,238
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: INHIBITORS (TITLE OF INVENTION: AND METHODS NUMBER OF SEQUENCES: 8
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221 S-----LDINFLSG-----SIPASLGNLNNLSFLYLYNNQLSGSIPEEIGYLRSLT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             445 KQLLMTKTGVTDYRFLDNMPQLEGIDISQNNLKDISFLSKYKN-------
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FILING DATE:
                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                         CALIFORNIA
C: UNITED STATES
                                                                                                                                                                                                                                 E: CAMPBELL AND FLORES
4370 LA JOLLA VILLAGE DRIVE,
                                                                                                                                                                                                                                                                                                                                                                                         WHITBY, DAVID J. HARPER, JOHN R.
                                                                                                                                                                                                                                                                                                                                                  PIERSCHBACHER, MICHAEL D.
BORDER, WAYNE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                RUOSLAHTI, ERKKI I.
LONGAKER, MICHAEL T.
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                                                                                                                                                                                                                                                                                                         INHIBITORS OF CELL REGULATORY FACTORS AND METHODS FOR PREVENTING OR REDUCING SCARRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
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                                                                                                                                                                                                                                   SUITE 700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-458-834-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08458834
; Patent No. 6277812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.8%; Score 155.5; DB 1; Length 359; Best Local Similarity 25.8%; Pred. No. 0.00029; Matches 93; Conservative 51; Mismatches 101; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                   APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: LONGAKER, MICHAEL T.
APPLICANT: WHITBY, DAVID J.
APPLICANT: HARPER, JOHN R.
APPLICANT: BORDER, JOHN R.
APPLICANT: BORDER, WAVER A.
APPLICANT: BORDER, WAVER A.
TITLE OF INVENTION: INHIBITORS OF CELL REGULATORY
TITLE OF INVENTION: AND METHODS FOR PREVENTING OR
                    ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TELEFAX: 619-535-8949
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FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
                                                                                                                                    STREET:
CITY: S
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                                                                   COUNTRY: UZIP: 92122
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    COMPUTER:
                                                                                                                 STATE:
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                                                                                                                                                                                ADDRESSEE:
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                                                                                                             SAN DIEGO
: CALIFORNIA
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I: Floppy disk
IBM PC compatible
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US-08-190-802A-50
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                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/08190802A Patent No. 5519003
                                                                                                                                                                                                                                                                                                                   Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,931
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-LA 9453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM: MEDIJUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 TALDI------LSVSKNQLTNV--NLSKPNKTVTNIDISHNNISL 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                            248 AKLGLSFNSISAVDNGSLANTPHLRELHLDNNKLTRVPGGLAE-HKY1QVVYLHNNNISV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 KLKQLLMTKTGVTDYRFLDNMPQLEGIDISQNNLKDISFLSKYKNLTLVAAADNGIEDIR 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 HLRVVQCSDLG------LDKVP------KDLP-----PDTTLLDLQNNKITEIK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                         COUNTRY: USA
ZIP: 94306-0850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                    STATE:
                                                                                                          CITY: Palo Alto
                                                                                                                             STREET:
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                                                                                                                                                 ADDRESSEE:
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Local Similarity 25.8%; Pred. No. 0.00029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMKKLS----YIRI-ADTN-----ITSIPQGLPPSLTELHLDGNKISRVDAASLKGLNNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLEGIEASSVIVRVEAEGNQIKSLVLKDKQG---SLTFLDVTGNQLT-----SLEGVNNF 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TLQELRAHENEI-----TKVRKVTFNGLNQMIVIELGTNP-LKSSGIENGAFQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSRNADVDLATLQAPKLETLMVNDTKVSHLDF-----LKNNPNLSSLSINRAQLQ 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93;
                                                                                      CA
                                                                                                                               P.O.
                                                                                                                                                                                                                                                        Ron,
                                                                                                                                                                                                                                                                            Mochly-Rosen, Daria
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                                                                                                                             Dehlinger & Associates
O. Box 60850
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                                                                                                                   US-08-477-346-50
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Sequence 50, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Deri
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 LNLQGSWLRSLEPQ-ALLGLQNLYYLHLERNRLRNLAVG------LFTHTPSLASLSLS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 LGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLSDIEIGKDIPDPHAIEHARELEKHKVG 355
                                                                                                                                                                                                   474 SAEVLGPLQRAFWLDISHNHLETLAE 499
                                                                                                                                                                                                                                        677 N--LSKPNKTVTNIDISHNNI-SLAD 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 LFCGLGELRELDLSRNALRSVK-ANVFVHLPRLQKLYLDRNLITAVAPGAFL-GMKALRW 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                      VEAEGNQIKSLVLKDKQGSLTFLDVTGNQLTSL----EGVNNFTALDILSVSKNQLTNV 676
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SYSTEM: PC-DOS/MS-DOS
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23.3%; Pred. No. 0.00089;
      WD-40 - Derived Peptides
                                                                                                                                                                                                                                                                                   -SELLELDLTTNRLTHLPRQLFQGLGH---LEYLLLSYNQLTTL
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pro. complex-rat, Fig. 33
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      Uses
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INFORMATION FOR SEQ ID NO:
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INDIVIDUAL ISOLATE:
            434 ---
                   622 VEAEGNQIKSLVLKDKQGSLTFLDVTGNQLTSL-----EGVNNFTALDILSVSKNQLTNV 676
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HYPOTHETICAL:
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LENGTH: 603 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/41
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                575 LETLMVNDTKVSHLD-------FLKNNPNLSSLSINRAQLQSLEGIEASSVIVR 621
                                                                                                                                                                                                                                                                          469 IDISQNNLKDI--SFLSKYKNLTLVAAADNGIEDIRP--LGQLPNLKFLVLSNNKISDLS 524
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                        331 ERTFEGLGQLEVLTLNDNQITEVRVGAFSGLFNVAVMNLSGNC---LRSLPERVFQGLDK 387
                                                                                                                                                                                                                                    271 LDLSHNRVAGLMEDTFPGLLGLHVLRLAHNAIASLRPRTFKDLHFLEELQLGHNRIRQLG 330
                                                                                                                                                                                                                                                                                                                  213 LFCGLGELRELDLSRNALRSVK-ANVFVHLPRLQKLYLDRNLITAVAPGAFL-GMKALRW 270
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                                                                                                                                                                                                                                                                                                                                                                                               155 SNLLGRL--EEGLFQGLSHLWDLNLGWNSLVVLPDTVFQGLGNLHELVLAGNKLTYLQPA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                     356 MDTLRALGFDEEVILDIVRTHDAPTPFPSNEKDPNMMKEWLATVIKLDLGSRK----DPL 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 LNLQGSWLRSLEPQ-ALLGLQNLYYLHLERNRLRNLAVG-----LFTHTPSLASLSLS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                              388 LHSLHLEHSCLGHVRLHTFAGLSGLRRLFLRDN-----SISSIEEQSLAGL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 LGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLSDIEIGKDIPDPHAIEHARELEKHKVG 355
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TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CITY: Washington
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                                                                                                                                                                                              --PLASLHOLQELHIDNNQITD--LSPVSHKESLTVVDLSRNADVDLATLQ-----APK 574
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pro. complex-rat, Fig. 33
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; INDIVIDUAL ISOLATE: Insulin-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
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ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
245 QKLYLDRNLIAAVAPGAFLGLKALRWLDLSHNRVAGLLEDTFP--GLLGLRVLRLSHNAI 302
                                     195 ------SLRELVLAGNRLAYLQPALFSGLAELRELDLSRNALRAIKANVFVQLPRL 244
                                                                                                                                                                                                                                                                          313 LGLEYPHHDHAHVLMLSDIEIGKDIPDPHAIEHARELEKHKVGMDTLRALGFDEEVILDI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 -
TITLE OF INVENTION: Thereof
                                                                                                                 433 KDISPVLQFKKLKQLLM--TKTGVTDYRFLDNMPQLEGIDISQNNLKDISF-----L 482
                                                                                                                                                                                             373 VRTHDAPTPFPSNEKDPNMMKEWLATVIKLDLGSRKDPLQRKGLSLLPNLETLGIGFTPI 432
                                                                                                                                                                                                                                           119 LGLENLCHLHLERNQLRSLALGTFAHTP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677 N--LSKPNKTVTNIDISHNNI-SLAD 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fabian, Gary R. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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CITY: Palo Alto
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                                                                                                                                                           ------LFEGLGSLWDLNLG------WNSLAVLPDAAFRGLG---- 194
                                                                                                                                                                                                                                                                                                                                            22.7%;
                                                                                                                                                                                                                                                                                                                  3.7%; Score 152.5; DB 1; Length 605; 22.7%; Pred. No. 0.0011; 1ve 62; Mismatches 151; Indels 131
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                                                                                                                                                                                                                                                                                                                         Indels 131;
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Search completed: December 3, 2001, 07:16:08 Job time: 137 sec

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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/paa/F
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3: /cgn2_6/ptodata/2/paa/U
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Listing first 45 summaries
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/ cgn2_6/ptodata/2/paa/US081_COMB.pep: *
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sequence 87, Ap	Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 85, Appli Sequence 85, Appli Sequence 85, Appli Sequence 84, Application Applied The Applied	Description

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,	Sequence 95, APP1	Sequence 94, APP1		000	70.7	ON Ar	8981	Sequence 11477, A	Sequence 98, Appi	Sequence 96, APPI	Sequence b, Appri	sequence o, appri	` _	Seducince			edition to	O	œ	o o	e 2, Appl	e 2	2	, a	equence 13,	equence 15, App	л ,	7 ,	9 6	6 83 . Ar	- 3396. A	e 6359, A	57, App	Œ	e 78, A	e 522	e 2, Apr	e 89,	æ	•

ALIGNMENTS

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CURRENT APPLICATION NUMBER: PCT/US00/23417
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: U.S. 60/150,750
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application PC/TUS0023417 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
PCT-US00-23417-4
                                                                                                                                                                               , ORGANISM: Streptococcus pyogenes PCT-US00-23417-4
                                                                           Query Match 100.0%; Score 4080; Best Local Similarity 100.0%; Pred. No. 0; Matches 792; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Johnson, Leslie S.
APPLICANT: Koenig, Scott
APPLICANT: Koenig, Scott
APPLICANT: Adamou, John E.
APPLICANT: Namou, John E.
TITLE OF INVENTION: Pneumococcal Protein Homologs and Fragments for
TITLE OF INVENTION: Vaccines
TITLE REFERENCE: 469201-402
                                                                                                                                                                                                                        LENGTH: 79
TYPE: PRT
Mismatches
                                                                                                                                      DB 1;
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APPLICANT: Adamou, John E.
TITLE OF INVENTION: Pneumococcal Protein Hol
TITLE OF INVENTION: Vaccines
FILE REFERENCE: 469201-402
CURRENT APPLICATION NUMBER: US/09/645,835
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: U.S. 60/150,750
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 6
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LENGTH: 792
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Koenig, Scott
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Sequence 4, Application US/09645835A; GENERAL INFORMATION:

APPLICANT: Heinrichs, Jon APPLICANT: Johnson, Leslie S. APPLICANT: Koenig, Scott APPLICANT: Adamou, John E.

US-09-645-835A-4

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; TYPE: PRT; ORGANISM: Streptococcus pyogenes US-09-645-835A-4
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Best Local :
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100.0%; Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: KOVATÍK, JOSEPH E.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 303/863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                           399 VIKLDLGSRK--DPLQRKGLSLLPNLETLGIGFTPIKDISPVLQFKKLKQLLMTKTGVTD 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                457 YRFLDNMPQLEGIDISQNNLKDISFLSKYKNLTLVAAADNGIEDIRPLGQLPNLKFLVLS 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
696 S 696
                                                                         636 DKQGSLTFLDVTGNQLTSLEGVNNFTALDILSVSKNQLTNVNLSKPNKTVTNIDISHNNI 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                     238 SGLTKLTELKLGANQISNISPLAGLTALTNLELNENQLEDISPISNLKNLTYLTLYENNI 297
                                                                                                                                                                                                                                                                          59 ITPLKDLTKLVDILMNNNQIADITPLANLTNLTGLTLFNNQITDIDPLKNLTNLNRLELS 118
                                                                                                                                                                                                                                                                                                                                                      2 ILKTVLGKTNVTDTVSQTDLDQVTTLQADRLG---IKSIDGLEYLNNLTQINFSNNQLTD 58
                                                                                                                 ESLIATUNQISDITPLGILTNLDELSLNGNQLKDIGTLASLTNLTDLDLANNQISNLAPL 237
                                                                                                                                                       ETLMVNDTKVSHLDFLKNNPNLSSLSINRAQLQSLEGIEASSVIVRVEAEGNQIKSLVLK 635
                                                                                                                                                                                            SNTISDISALSGLTNLQQLSF-GNQVTDLKPLANLTTLERLDISSNKVSDISVLAKLTNL 177
                                                                                                                                                                                                                                  NNKISDLSPLASLHOLOELHIDNNQITDLSPVSHKESLTVVDLSRNADVDLATL-QAPKL 575
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Potter, Terry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
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; ORGANISM: S. pneumoniae
US-09-471-255-86
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APPLICANT: BRODER, Bernard R.
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
APPLICANT: RIOUX, Cl.ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT APPLICATION NUMBER: US/09/471,255
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SEQ ID NO 86
LENGTH: 1019
           ~ 519 -KISDLS-PLASLHQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/113,800 PRIOR FILING DATE: 1998-12-23 NUMBER OF SEQ ID NOS: 102
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                                           678 TFTVPTSLAYKMASQTIFYPFHAGDTYLR-VNPQFAVPKGTDALVRVFDEFHGNAYLENN 736
                                                                                   484 KYKNLTLVA------AADNGIEDIRPLGQLP-NLKFLV-----LSNN 518
                                                                                                                                 618 NMLVKLITPDGKVLEKVSGKVFGEGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDG 677
                                                                                                                                                                               568 GNKYYTGEELTNYVNL---LKNSTFNNQNFTLANGQKRVSFSFPPELE------KKLGI 617
                                                                                                                                                                                                                                                                  389 PNMM--KEWLATVIKLDLGSRKDFLQRKGLSLLFNLETLGIGFTFIKDISFVLQFKKLKQ 446
                                                                                                                                                                                                                                                                                                                534 ------HHADPIDEHKPVG------IGHSHSNYELFKPEEGVAKKE 567
                                                                                                                                                                                                                                                                                                                                                           334 GKDIPDPHAIEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPFPSNE----KD 388
                                                                                                                                                                                                                                                                                                                                                                                                         488 NAKEMKDLDKKIEEKIAGIMKQYGVKRESI---VVNKEKNAIIYPHGDH------ 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 --PELSEREKEYQEKLAYLAEKLGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLSDIEI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 VMSHGDHNHYFFKKDLTE------EQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPS 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 LVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEKPAETHQT------ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH----EKHEEDGYGFDANRIIAEDESGF 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 KSSLSGQTQAQAKQVATRLPQTSSLVSTATANGIPGLHFPTSDGFQFNGQGIVGVTKDSI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 AKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIVAEDALGYTVRHDDHFHYIL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 ESDGLVF-DPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 SQLSYSSTASDNN-----TQSVAKGSTS---KPANKSENLQSLLKEL--YDSPSAQRYS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 -DDGFILTKDSKILSKTDQGIVVDHDGHSHFIFYADLKG--SPFEYLIP---KGARB--- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 SQLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT---- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Match 7.3%; Score 297.5; DB 18; Length 1019; Local Similarity 21.5%; Pred. No. 3.2e-13; Local Similarity 114; Mismatches 286; Indels 277; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113,800
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 1019
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APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, JOS, e
APPLICANT: HADDEUR, Bernard R.
APPLICANT: HADDEUR, Learnard R.
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
APPLICANT: MOUX, Cl, ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
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484 DYPGNAKEMKDLDKKIEEKIAGIMKQYGVKRESI---VVNKEKNAIIYPHGDH----- 533
                                            276 -----PELSEREKEYQEKLAYLAEKLGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLS 329
                                                                                              434 ESGFIMSHGNHNHYFFKKDLTE------EQIKAAQKHLEEVKTSHNGLDSLSSHEQ 483
                                                                                                                                                                                             383 IPKSNQIGQPTLPNNSLAT--PSPSLPIN-----PGISHEKHEEDGYGFDANRIIAED 433
                                                                                                                                              229 KDSILVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEKPAETHQT------ 275
                                                                                                                                                                                                                                            171 ILKSSLSGOTQAQAKQVATRLPQTSSLVSTATANGIPGLHFP--TSDGFQFNGQGIVGVT 228
                                                                                                                                                                                                                                                                                            323 TNAKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHY 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 SQLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT----- 70
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; LENGTH: 1019
; TYPE: PRT
; ORGANISM: S.
US-09-471-255-55
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APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, Jos,e
APPLICANT: BRODEUR, Bernard R.
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                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MARTIN, Denis
APPLICANT: RIOUX, C1,ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/113,800
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 3
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             907
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ESDGLVF-DPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTN 324
                                    -DDGFILTKDSKILSKTDQGIVVDHDGHSHFIFYADLKG--SPFEYLIP---KGASL--- 121
                                                                                                  SQLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT-----
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                                                                         SQLSYSSTASDNN-----TQSVAKGSTS---KPANKSENLQSLLKEL--YDSPSAQRYS
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                                                                                                                                                          Conservative 114; Mismatches
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                                                                                                                                                                                                                                                                                  Sequence 84, Application US/09471255
GENERAL INFORMATION:
APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL JOS, e
APPLICANT: BRODEUR, Bernard R.
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 84
                                                                                                                      CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
                                                                                                                                                                APPLICANT: BRODEUR, Bernard R.
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: RIOUX, CL.ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
                                                                       PRIOR APPLICATION NUMBER: US 60/113,800 PRIOR FILING DATE: 1998-12-23
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GKVSTGTVENQPT-ENKPADSLPEA 932
                                    SMVGNGTAEEKAAMATKAKESAQEA 746
                                                                                                                                                                                  VIVRVEAE-----GNQIKSLVLKD------KQGSLTFLDVTG-----NQLTSLEGVNNFT
                                                                                                                                                                                                                                                                                           YKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEV-PILEKENQT-----
                                                                                                                                                                                                                                                                                                                                                                                                      KYKNLTLVA-------AADNGIEDIRPLGQLP-NLKFLV-----LSNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -DDGFILTKDSKILSKTDQGIVVDHDGHSHFIFYADLKG--SPFEYLIP---KGASL--- 12:
                                                                                                          ALDILSVSKNOLTNVNLSKPNKTVTNIDISHNNISLADLKLNEQHIPEAIAKNFPAVYEG
                                                                                                                                                TSEKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNMM--KEWLATVIKLDLGSRKDPLQRKGLSLLPNLETLGIGFTPIKDISPVLQFKKLKQ 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKDIPDPHAIEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPFPSNE----KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --PELSEREKEYQEKLAYLAEKLGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLSDIEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMSHGDHNHYFFKKDLTE------EQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEKPAETHQT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSNQIGQPTLPNNSLAT -- PSPSLPINPGTSH -- -- EKHEEDGYGFDANRIIAEDESGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSSLSGQTQAQAKQVATRLPQTSSLVSTATANGIPGLHFPTSDGFQFNGQGIVGVTKDSI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESDGLVF-DPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTN
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                                                                                                                                                                                                                                                                                                                                                                   TFTVPTSLAYKMASQTIFYPFHAGDTYLR-VNPQFAVPKGTDALVRVFDEFHGNAYLENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLMTKTGVTDYRFLD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNKVYTGEELTNVVNL---LKNSTFNNQNFTLANGQKRVSFSFPPELE-----KKLGI
                                                                                                                                                                                                                     -----DKPSILPQFKRNKAQENSKFDEKVEEPK
                                                                                                                                                                                                                                                       RNADVDLATLQAPKLETLMVNDTKVSHLDFLKNNPN-LSSLSINRAQLQSL--EGIEASS
                                                                                                                                                                                                                                                                                                                               NMLVKLITPDGKVLEKVSGKVFGEGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IGHSHSNYELFKPEEGVAKKE 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 292.5; DB 18; Length 1019; ilarity 21.4%; Pred. No. 7.8e-13; Conservative 114; Mismatches 283; Indels 283;
                                                                        ----TIELYLPSGEV----IKKN---MADF---TGEAPQGNGENKPS--EN
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RESULT 9 US-09-471-255-87

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RNADVDLATLQAPKLETLMVNDTKVSHLDFLKNNPN-LSSLSINRAQLQSL--EGIEASS 617

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; LENGTH: 1019
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GENERAL INFORMATION:
APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, Jos.e
APPLICANT: BRODEUR, Bernard R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 87
LENGTH: 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/113,800 PRIOR FILING DATE: 1998-12-23 NUMBER OF SEQ ID NOS: 102 SOFTWARE: FastSEQ for Windows Version 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PINEAU, Isabelle APPLICANT: MARTIN, Denis APPLICANT: RIOUX, Cl,ment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEKPAETHQT---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKP------AVAQRAASQGTSK-VADPHHHYEFNPADIVAEDALGYTVRHDDHFHYIL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESDGLVF-DPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT----
YKYGEIKLPIPKLNQGTTRTAGNKIPYTFMANAYLDNQSTYIVEV-PILEKENQT-----
                                                                                     TFTVPTSLAYKMASQTIFYPFHAGDTYLR-VNPQFAVPKGTDALVRVFDEFHGNAYLENN
                                                                                                                                                                                                                 LLMTKTGVTDYRFLD-----
                                                                                                                                                                                                                                                        GNKVYTGEELTNVVNL---LKNSTFNNQNFTLANGQKRVSFSFPPELE-----KKLGI 617
                                                                                                                                                                                                                                                                                                                                                                   GKDIPDPHAIEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPFPSNE----KD 388
                                                                                                                                                                                                                                                                                                                                                                                                                         NAKEMKDLDKKIEEKIAGIMKQYGVKRESI----VVNKEKNAIIYPHGDH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PELSEREKEYQEKLAYLAEKLGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLSDIEI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMSHGDHNHYFFKKDLTE------EQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPG
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                                           -KISDLS-PLASLHQ---
                                                                                                                                                                          NMLVKL1TPDGKVLEKVSGKVFGEGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSNQIGQPTLPNNSLAT -- PSPSLPINPGTSH----EKHEEDGYGFDANRIIAEDESGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185;
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                                                                                                                              ----AADNGIEDIRPLGQLP-NLKFLV------LSNN 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                           ---LQELHIDNNQ--ITDLSPVSHKESLTVVDLS
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                                                                                                                                                                                                                                                                                                                                           - IGHSHSNYELFKPEEGVAKKE 567
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 88
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Best Local Similarity
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CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BRODEUR, Bernard R.
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: RIOUX, Cl,ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1019
TYPE: PRT
ORGANISM: S. pneumoniae
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APPLICANT: HAMEL, Jos, e
389 PNMM--KEWLATVIKLDLGSRKDPLQRKGLSLLPNLETLGIGFTPIKDISPVLQFKKLKQ 446
                                                                                334 GKDIPDPHAIEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPFPSNE----KD 388
                                                                                                                                         488 NAKEMKOLDKKIEEKIAGIMKQYGVKRESI---VVNKEKNAIIYPHGDH------
                                              534 -----HHADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 567
                                                                                                                                                                                                                               438 VMSHGDHNHYFFKKDLTE------EQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPS 487
                                                                                                                                                                                                                                                                             233 LVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEKPAETHQT---------
                                                                                                                                                                                                                                                                                                                         385 KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH-----EKHEEDGYGFDANRIIAEDESGF 437
                                                                                                                                                                                                                                                                                                                                                                        173 KSSLSGQTQAQAKQVATRLPQTSSLVSTATANGIPGLHFPTSDGFQFNGQGIVGVTKDSI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIVAEDALGYTVRHDDHFHYIL 172
                                                                                                                                                                                276 --PELSEREKEYQEKLAYLAEKLGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLSDIEI 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 -DDGFILTKDSKILSKTDQGIVVDHDGHSHFIFYADLKG--SPFEYLIP---KGASL--- 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 SQLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT---- 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 114; Mismatches
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CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113,800
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 89
LENGTH: 1019
TYPE: PRT
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                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 89, Application US/09471255 GENERAL INFORMATION:
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APPLICANT: RIOUX, C1,ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, Jos,e
APPLICANT: BRODEUR, Bernard I
APPLICANT: PINEAU, Isabelle
                                             122 AKP-----AVAQRAASQGTSK-VADPHHHYEFNPADIVAEDALGYTVRHDDHFHYIL 172
325 AKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 384
                                                                                               266 ESDGLVF-DPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTN 324
                                                                                                                                                                                               217 SQLSYSSTASDNN-----TQSVAKGSTS---KPANKSENLQSLLKEL--YDSPSAQRYS 265
                                                                                                                                             71 -DDGFILTKDSKILSKTDQGIVVDHDGHSHFIFYADLKG--SPFEYLIP---KGASL--- 121
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                                                                                                                                                                                                                                                  16 SQLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDFPT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 -KISDLS-PLASLHQ-------LQELHIDNNQ--ITDLSPVSHKESLTVVDLS 560
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                                                                                                                                                                                                                                                                                                               185;
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                                                                                                                                                                                                                                                                                                  Conservative 114; Mismatches 283; Indels 283; Gaps
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; TYPE: PRT ; ORGANISM: S. pneumoniae US-09-471-255-2
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                                                                                    SOFTWARE: 1
SEQ ID NO 2
                                                                                                                                                                                                                               APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, Jos,e
APPLICANT: BRODEUR, Bernard R.
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: RIOUX, C1,ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113,800
PRIOR FILING DATE: 1998-12-23
                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                   LENGTH: 1039
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                                                                                                           FastSEQ
                                                                                                             for Windows Version 3.0
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RESULT 13
US-09-583-110-5226
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 -DDGFILTKDSKILSKTDQGIVVDHDGHSHFIFYADLKG--SPFEYLIP---KGASL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KISDLS-PLASLHQ-------LQELHIDNNQ--ITDLSPVSHKESLTVVDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMLVKLITPDGKVLEKVSGKVFGEGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDG 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNKVYTGEELTNVVNL----LKNSTFNNQNFTLANGQKRVSFSFPPELE------KKLGI 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKDIPDPHAIEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPFPSNE----KD 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAKEMKDLDKKIEEKIAGIMKQYGVKRESI---VVNKEKNAIIYPHGDH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMSHGDHNHYFFKKDLTE------EQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFTVPTSLAYKMASQTIFYPFHAGDTYLR-VNPQFAVPKGTDALVRVFDEFHGNAYLENN 756
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                                                                                                                                                                                                                           ALDILSVSKNQLTNVNLSKPNKTVTNIDISHNNISLADLKLNEQHIPEAIAKNFPAVYEG
                                                                                                                                                                                                                                                                           TSEKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDG-----
                                                                                                                                                                                                                                                                                                                   VIVRYEAE-----GNQIKSLVLKD------KQGSLTFLDVTG----NQLTSLEGVNNFT 661
                                                                                             GKVSTGTVENQPT-ENKPADSLPEA
                                                                                                                                          SMVGNGTAEEKAAMATKAKESAQEA 746
                                                                                                                                                                                     -----TIELYLPSGEV----IKKN---MADF---TGEAPQGNGENKPS--EN
                                                                                                                                                                                                                                                                                                                                                                                                           RNADVDLATLQAPKLETLMVNDTKVSHLDFLKNNPN-LSSLSINRAQLQSL--EGIEASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEV-PILEKENQT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----AADNGIEDIRPLGQLP-NLKFLV-----LSNN
                                                                                               952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NMPQLEG----IDISQNNLKDISFLS 483
                                                                                                                                                                                                                                                                                                                                                                        ---DKPSILPQFKRNKAQENSKLDEKVEEPK
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Sequence 5226, Application US/09583110 GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and TITLE OF INVENTION: Pneumoniae for Di

Nucleic Acid and Amino Acid Sequences Relating to Streptococc Pneumoniae for Diagnostics and Therapeutics

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 5226
LENGTH: 1039
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/085,131 PRIOR FILING DATE: 1998-05-12
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839 TSEKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLFNMDG----- 893
                                         618 VIVRVEAE-----GNQIKSLVLKD------KQGSLTFLDVTG----NQLTSLEGVNNFT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                       811 -----DKPSILPQFKRNKAQENSKLDEKVEEPK 838
                                                                                                                                   561 RNADVDLATLQAPKLETLMYNDTKVSHLDFLKNNPN-LSSLSINRAQLQSL--EGIEASS 617
                                                                                                                                                                               757 YKVGEIKLPIPKLNQGTTRTAGNKIPVTFMANAYLDNQSTYIVEV-PILEKENQT----- 810
                                                                                                                                                                                                                           519 -KISDLS-PLASLHQ-------LQELHIDNNQ--ITDLSPVSHKESLTVVDLS 560
                                                                                                                                                                                                                                                                                                                                                              638 NMLVKLITPDGKVLEKVSGKVFGEGVGNTANFELDQPYLPGQTFKYTTASKDYPEVSYDG 697
                                                                                                                                                                                                                                                                         698 TFTVPTSLAYKMASQTIFYPFHAGDTYLR-VNPQEAVPKGTDALVRVFDEFHGNAYLENN 756
                                                                                                                                                                                                                                                                                                                   484 KYKNLTLVA-------AADNGIEDIRPLGQLP-NLKFLV-----LSNN 518
                                                                                                                                                                                                                                                                                                                                                                                                          447 LLMTKTGVTDYRFLD--------NMPQLEG----IDISQNNLKDISFLS 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                         588 GNKYYTGEELTNYVNL---LKNSTFNNQNFTLANGQKRVSFSFPPELE-----KKLGI 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389 PNMM--KEWLATVIKLDLGSRKDPLQRKGLSLLPNLETLGIGFTPIKDISPVLQFKKLKQ 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   554 -----HADPIDEHKPVG-----IGHSHSNYELFKPEEGVAKKE 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 NAKEMKDLDKKIEEKIAGIMKQYGVKRESI---VVNKEKNAIIYPHGDH----- 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 --PELSEREKEYOEKLAYLAEKLGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLSDIEI 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 VMSHGDHNHYFFKKDLTE------EQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPG 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 AKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 SQLSYSSTASDNN-----TQSVAKGSTS---KPANKSENLQSLLKEL--YDSPSAQRYS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 -DDGFILTKDSKILSKTDQGIVYDHDGHSHFIFYADLKG--SPFEYLIP---KGASL--- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 SQLTLIACQSRGNGTYPIKTKQSRKGMTSNKIKPIKKSKKTNKTHKGVAGVDEPT---- 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH-----EKHEEDGYGFDANRIIAEDESGF 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.0%; Score 287; DB 18; Length 780; Best Local Similarity 25.6%; Pred. No. 1.3e-12; Matches 123; Conservative 63; Mismatches 166; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, Jos,e
APPLICANT: BRODEUR, Bernard R.
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL STREPTOCCCCUS ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 12806-11PCT
CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
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568 GNKYYTGEELTNYVNLLKNSTFNNONFTLANGOKRVSFSFPPELEKKLGINML-VKLITP 626
                                          389 PNMM--KEWLATVIKLDLGSR------KDPLQRKGLSLLPNLE-TLGIGFTPIKDISP 437
                                                                                         534 -----HADPIDEHKPVG------IGHSHSNYELFKPEEGVAKKE 567
                                                                                                                                      334 GKDIPDPHAIEHARELEKHK-VGMDTLRALGFDEEVILDIVRTHDAPTPFPSNE----KD 388
                                                                                                                                                                                   488 NAKEMKDLDKKIEEKIAGIMKQYGVKRESI---VVNKEKNAIIYPHGDH------ 533
                                                                                                                                                                                                                                                                             438 VMSHGDHNHYFFKKDLTE-------EQIKAAQKHLEEVKTSHNGLDSLSSHEQDYPG 487
                                                                                                                                                                                                                                276 --PELSEREKEYQEKLAYLAEKLGIDPSTIKRVETQDGKLGLEYPHHDHAHVLMLSDIEI 333
                                                                                                                                                                                                                                                                                                                            233 LVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEKPAETHQT------
                                                                                                                                                                                                                                                                                                                                                                       385 KSNQIGOPTLPNNSLAT---PSPSLPINPGTSH-----EKHEEDGYGFDANRIIAEDESGF 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 AKPNEVVSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIP 384
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APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, Jos,e
APPLICANT: HAMEL, Jos,e
APPLICANT: BRODEUR, Bernard R.
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
APPLICANT: MOVEL STREPTOCOCCUS ANTIGENS
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
TITLE REFERENCE: 12806-11PCT
CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-3
PRIOR APPLICATION NUMBER: US 60/113,800
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LENGTH: 489
; TYPE: PRT
; ORGANISM: S. pneumoniae
US-09-471-255-56
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Search completed: December 3, 2001, 07:22:27 Job time: 516 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.1%; Score 248.5; DB 18; Length 489; Best Local Similarity 28.9%; Pred. No. 5.8e-10; Matches 86; Conservative 42; Mismatches 113; Indels 57; Gaps
                                                                                                                                                                                                                                                                                                                     217 SQLSYSSTASDNN-----TQSVAKGSTS---KPANKSENLQSLLKEL--YDSPSAQRYS 265
                                                                                                                                                                                                                       385 KSNQIGQPTLPNNSLAT--PSPSLPINPGTSH----EKHEEDGYGFDANRIIAEDESGF 437
                                                                                                                                                                                                                                                                   173 KSSLSGQTQAQAKQVATRLPQTSSLVSTATANGIPGLHFPTSDGFQFNGQGIVGVTKDSI 232
                                                                                                                                                                                                                                                                                                                                                                                                                        266 ESDGLVF-DPAKIISRTPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTN 324
                                                                                                                          438 VMSHGDHNHYFFKKDLTE-----EQIKAAQKHLEEVKTSHNGLDSLSSHEQDY 485
                                                                                                                                                                        233 LVDHDGHLHPISFADLRQGGWAHVADQYDPAKKAEKPAETHQT-----PELSEREKEY 285
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Result
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US-08-108-804-3
US-08-108-804-3
US-08-956-291-3
PCT-US95-10661A-3
US-08-96-791-6
PCT-US95-10661A-6
US-08-663-112-2
US-08-663-112-2
US-08-488-940-2
US-09-080-855-12
PCT-US94-09943-2
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Sequence 66, Appl Sequence 182, Appl Sequence 11, Appl Sequence 11, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 21, Appli Sequence 30, Appli Seque
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RESULT 1 US-08-961-083-66 Sequence 66, Application US/08961083 Patent No. 6159469 Patent No. 6159469 REPLICANT: Chol et. al. APPLICANT: Chol et. al. APPLICANT: Chol et. APPLICANT: Chol et. ITILE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines INUMER OF SEQUENCES: 452 CORRESSONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 key West Avenue CITY: ROCKVILLE STATE: MARYLAND IPI: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: BRADABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOPTWARE: ASCII Text CURRUM APPLICATION NUMBER: US/08/961,083 CLASSIFICATION ANDA: APPLICATION NUMBER: US/08/961,083 PILING DATE: APPLICATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB340P2 TELECOMMUNICATION INFORMATION: REFERENCE/DOCKET NUMBER: B9340P2 TELECHAM: (301) 309-85504 TE	28 124 2.8 2366 2 US-08-495A-10 Sequence 10, App 123.5 2.8 1194 2 US-08-488-940-17 Sequence 17, App 31 123.5 2.8 1194 2 US-08-488-940-17 Sequence 18, App 123.5 2.8 1194 2 US-08-488-940-17 Sequence 18, App 132 122 2.8 1545 4 US-08-96-791-4 Sequence 4, Appl 134 121.5 2.8 1702 4 US-08-96-791-5 Sequence 5, Appl 135 121.5 2.8 1702 5 PCT-US95-10661A-5 Sequence 5, Appl 136 121 2.8 682 3 US-08-96-10661A-5 Sequence 5, Appl 137 121 2.8 682 3 US-08-613-009A-10 Sequence 9, Appl 138 119 2.7 542 1 US-08-96-791-25 Sequence 2, Appl 2.7 542 3 US-08-613-009A-2 Sequence 2, Appl 2.7 702 2 US-08-68-791-25 Sequence 2, Appl 2.7 702 4 US-09-074-658-19 Sequence 25, Appl 44 114.5 2.6 694 1 US-08-309-420-2 Sequence 19, App 2.7 1076 4 US-09-074-658-19 Sequence 19, App 2.7 1076 4 US-09-074-658-19 Sequence 27, Appl 2.7 1076 1076 1076-1076-1076-1076-1076-1076-1076-1076-
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                                                                                                                                                                          Sequence 56, Application US/08961083 Patent No. 6159469 GENERAL INFORMATION:
                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                  TITLE OF INVENTION: Streptococcus pneumoniae NUMBER OF SEQUENCES: 452
                                                                                                                                                       APPLICANT: Choi et. al.
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                  STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/961,083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYELGLYQARTVKENNRVSYID----GKQATQKTENLTPDEVSKREGINAEQIVIKITDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYQLGKHHMGLATKDNQIAYIDDSKGKVKAPKT-NKTMDQISAEEGISAEQIVVKITDQG
                                                                                                                                                                                                                                                         -RYLAG-----
                                                                                                                                                                                                                                                                                          QLYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIP 332
                                                                                                                                                                                                                                                                                                                                                                    QNSDNTSRTNWVPSVS-NPGTTNTNTSN-----NSNTNSQASQSND-----IDSLLK
                                                                                                                                                                                                                                                                                                                                                                                                TPAPGRRKAP-IPDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLD 317
                                                                                                                                                                                                                                                                                                                                                                                                                                        IFSPTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRG--ARPSDYRP
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DEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAY 572
                                                                                                           ------GKGLD---
                                                                                                                                              GISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHK 452
                                                                                                                                                                                                                    LRYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVGEGYVFEEK 392
                                                                                                                                                                                                                                                                                                                            QLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELAD---
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                                                                       ALFXNKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTE 512
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                                   -YDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANW 467
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US-08-961-083-182
Query Match
Best Local S
Matches 180
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                                                                                                                                                                                              TELEFAX: (301) 309-85 INFORMATION FOR SEQ ID NO:
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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 Local Similarity
nes 180; Conserv
                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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19.2%; Score 839.5;
40.7%; Pred. No. 1e-
tive 58; Mismatches
                                                                                                                                                                                                                                                                         36,373
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                le-61;
                                DB 4;
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                                Length 447;
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PCT-US93-07261-11
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                                                                                                                                                  APPLICATION NUMBER: US 07/927,531
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0288K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-822-7398
                                                                                                              TELEFAX: 201-82
INFORMATION FOR SEQ
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CORRESPONDENCE ADDRESS:
ADDRESSEE: John H. C. Blasdale
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Wo CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                MOLECULE TYPE: protein
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               FILING DATE: 19930800 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Madison
STATE: New Je:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                   TOPOLOGY:
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                                                                       LENGTH:
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RESULT 5
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                                                                                                LEEYNETDLAKGKEVTNKARENLEEYN 833
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Qy 390 HSKPSDKEVTHTFLGHRIKAYGKGLDGKPYDT 421	Db 332 SDDKVVVPVNKNKSSEPDKERAPDKKRTMEYRLSELEPI-VPRKDNELAVCGDSMD 386	QY 331 EDGLIFEPTQVIKSN-AFGYVVPHGDHYHIIPRSQLSPLEMELADRYLAGQTDDNDSGSD 389	Db 293 RILVK	QY 271 DVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLDQLHRLDLKYRHVE 330	Db 234 VETKFYGMRENALGELD-EYEERYEKKRYYLKEDGEGDLKDVEEKLEETGYGFREKFPTT 292	GNHYHYIPKKDLSPSELAAAQAYWSC	Db 174 SAINELKERRASRRPMMVKMQRGMKDEVDEWIKKYDDEQAEKNGTKDEEIKDKGDGYEEI 233	NEAKR	Db 114 PESVEKDLKEMELKEKEFIKQHLKDYEERKEKRRNWILRSLRRDKLREIEQLEKLNAQLE 173	QY 142 PGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSKEEV 182	Db 68NKETLKKKELENQKEKEEKNKIKDNNDEALKNKGNDKKIVPKK 113	QY 89 YHFYNGKVPYDAIISEELLMTDPNYHFKQSDVINEILDGYVIKVNGNYYYYLK 141	Db 11 TEKNEKARNALKEKKLKEQKKNDAQKAKDLTKKESQDSSSEKSLKEKVNGEALKEKE 67	OY 34 TKDNQIAYIDDSKGKVKAPKTNKTMDQISAEEGISAEQIVVKITDQGYVTSHGDH 88	Query Match 3.4%; Score 150.5; DB 5; Length 1663; Best Local Similarity 19.7%; Pred. No. 0.002; Matches 183; Conservative 137; Mismatches 364; Indels 243; Gaps	PONDENCE ADDRESS PONDENCE JUDIO H ESSEE: John H. ET: One Giralda : Madison O7940-1000 M TYPE: Floppy MARE: Microsoft ATING SYSTEM: Microsoft T APPLICATION DATA ICATION NUMBER: 10930A ICATION NUMBER: 10930A APPLICATION DATA ICATION NUMBER: 107-AUG ESTRATION NUMBER: 07-AUG Blasdale, Joh RENCE/DOCKET NUM MMUNICATION NIMBER: 201-822-70 FON SEQ ID N TE CHARACTERISTI- E TYPE: Deptid AL SOURCE: NISM NISM: Plasmodiu NISM: Plasmodiu NISM: Plasmodiu NISM: Plasmodiu NISM: Plasmodiu NISM: Plasmodiu	; GENERAL INFORMATION: ; TITLE OF INFORMACES: 23 : NUMBER OF SCOURNCES: 23
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US-08-596-291-3
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                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
RAPPLICATION UNMBER: US 08/
FILING DATE: 01-SEP-1993
ATTOREY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HERRIK
TITLE OF INVENTION: PRIMARY STI
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: TYROSINE PI
                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 09-AUG-19
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CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: LO4
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02210
                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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SARAS, JAN
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                                                                                                                           us 08/115,573
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1422 GQVVHLLLEK--GQSPTSKEHVPVTPQCTLSDQNA---QGQGPEKVKKTTQVKDYSFVTE 1476
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                                                                                                                            1997 -ISYPKGKCSTYQIKGSPNLTLPKESYIQEDDIY-----DDSQEAEVIQSLLDVVD-EEA
                                                                                                                                                                                                                                                                                                    1914 VNGVSTQGMTLEEVNRALDM-SLP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 SVDKSGVTAKHGDHFHYIGFGELEQYELDEVANWVKAKGQADELVAALDQEQGKEKPLFD 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 DRYLAGOTDDNDSGSDHSKPSDKEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIH 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 DQLHRLDLKYRHVEEDGLIFE-PTQVIKSN--AFGYVVPHGDHYHIIPRSQLSPLEMELA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 RPTPAPGRRKAPIPDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 PTDIIDDLGDAYL-----VPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDY
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QPSEA----SKEEKESDDFI----DSLPDYGLDRATLED 777
                                                                                         QELLAKKN-AGDA----
                                                                                                                                                                                                                   VVPSSKRSAVSAPKSTKGNGSYSVGSCSQPALTPNDSFSTV-----AGEEINE-----
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                                            QNLLNENNAAGDSCGPGTLKMNGKLSEERTEDTDCDGSPLPEYFTEATKMNGCEEYCEEK 2109
                                                                                                                                                                     RFAAPDGYIF-----DPRDVLAKETFVWKDGSFSIPRADGSSLRTINKSDLSQAEWQQA 715
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617/720-2441
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-100-804-3
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                                                                                                                                                                                                                                                                                       Query Match 3.1%; Score 135.5; DB 3; Length 2465; Best Local Similarity 19.6%; Pred. No. 0.067; Matches 172; Conservative 114; Mismatches 328; Indels 265; Gaps
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1535 L----KVNG---ASLKGLSQQEVISALRGTAPEVFLLLCRPPPGVLPEIDTALLTPLQS 1586
                                                                                                                                                                                        1422 GQVVHLLLEK--GQSPTSKEHVPVTPQCTLSDQNA---QGQGPEKVKKTTQVKDYSFVTE 1476
                                                                                                 1477 ENTFEVKLFKNSSGLGFSFSRED--NLIPEQINASIVRVKKLFAGQPAAESGKIDVGDVI 1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino aci
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CLASTIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/596,291
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
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APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
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                                                 125 LDGYVIKVNGNYYVYLKPGSKRKNIRT------
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FILING DATE: 09-AUG
APPLICATION NUMBER:
FILING DATE: 01-SEP-
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REFERENCE/DOCKET NUMBER: LO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617-720-2441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                               EGISAEQIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYHFKQSDYINEI 124
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IUMBER: US 08/115,573
01-SEP-1993
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                                                 -----KQQ 154
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	SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:	٠. ٠.	
	SYSTEM: PC-DOS/MS-DOS		
	PE: Floppy disk		
	COUNTRY: United ZIP: 94111-4187		
	San Francisco California	•• ••	
	ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400	٠. ٠.	
	NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:	٠. ٠.	
	OF INVENTION: H	٠. ٠.	
	CANT: Falkow, Stanley	٠. ٠	
	INFORMATION:	 	
	29 + en	US-08-	
	ZIIV VASESHIQAFQEAAIDUDEIIWGNDEHFIEKINHED Z145		
	47 QPSEASKEEKESDDFIDSLPDYGLDRATLED 777	P 9	
2109	2050 QNILLNENNAAGDSCGPGTLKMNGKLSBERTEDTDCDGSPLPEYFTEATKMNGCEEYCEEK	Db	
746	716 QELLAKKN-AGDAENQ	Qy	
2049	1997 -ISYPKGKCSTYQIKGSPNLTLPKESYIQEDDIYDDSQEAEVIQSLLDVVD-EEA	Db	
715	662 REAAPDGYIEDPRDVLAKETEVWKDGSFSIPRADGSSLRTINKSDLSQAEWQQA	QУ	
1996	1949 VPSSKRSAVSAPKSTKGNGSYSVGSCSQPALTPNDSFSTVAGEEINE	Db	
661	603 TIKYVMQHPEVRPDVWSKPGHEESGSVI-PNVTPLDKRAGMPNWQIIHSAEEVQKALAEG	Qy	
1948	1914 VNGVSTQGMTLEEVNRALDM-SLPSLVLKATRNDLP	Db	
602	SSAG	Qу	
1913	1854 NTNVASFATGHKLTCNKEELGFSLCGGHDSLYQVVYISDINPRSVAAIEGNLQLLDVIHY	Db	
545	494 TKKVSRKVT-KDGKVGYIMPKDGKDYFYARYQLDLTQIAFAEQELMLKDKKHY	Qy	
1853	1819 DTDVTNMTHTDGRVPRITQ	DЬ	
493	ä	Qy	
1818	1791 GCYVHDVIQDPAKSDGRLKPGDRLIKVN	Db	
433	374 DRYLAGGTDDNDSGSDHSKPSDKEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIH	Qy	
1790	1748 TPL-KNDLE-NHLEDFELEVELLITLIKSEKASLGFTVTKGNQRI	Db	
373	YRHVEEDGLIFE-PTQVIKSNAFG	Qy	
1747	1704 NPSPLPPDMAPGQSYQPQSESASSSSMDKYHIHHISEPTRQENW	Db	
316	ÀΡ	Qy	
7	1647 PANISNSTWSSALHQTLSNMVSQAQSHHEAPKSQEDTICTMFYYPQKIPNKPEFEDS	Db	
σ.	204 PTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGARPSDY	Оу	
164	1587 PAQVLPNSSKDSSQPSCVEQSTSSDENEMSDKSKKQCKSPSRRDSYSDSSGSGEDDLVTA	DЬ	
203	QVAKGT	VΥ	

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Best Local 9
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
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REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 38-3249
TELEFAX: (415) 781-77000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                      1012 -----SNNEEIARVDEAPVPPPAPAT-------PSETTETVAENSKQESKTVE 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      462 DNKGSLKVGDGTVILKQQTNGSGQHAFASVGIVSGRSTLVLNDDKQVDPNSIYFGFRGGR 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 NAFGYVVPHGD------HYHIIPRSQLSPLEMELADRYLAGQTDDNDSGSDHSKPSD 395
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631 PNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFAAPDGYIFDPRDVLAKETFVWKDGSFS 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 NHINNERMNGFNGYFGEEEGKNNGNLNVTFKGKSE------QNRFLLTGG-----TN 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 K------GTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGYIFSPTD 206
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                                                                                                                                                                                                                                                                 906 LSNKQGDKVVVTKSATGNFTLQVADKTGEPNHNELTLFDASKAQRDHLNVSLVGNTVDLG 965
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                                                                                                                    571 NATYDTGSSFVIPHIDHIHVVPYSWLTRNQIATIKYVMQHPEVRPDVWSKPGHEESGSVI 630
                                                                                                                                                                    966 AWKYKLRNVNGRYDLYNPEV-----EKRNQTVDTTNITTPNNIQADVPSVP---- 1011
                                                                                                                                                                                                                 515 GKDY----FYARYQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAG 570
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                                                                                                                                                                                                                                                                                                                                                                                                            KEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGE 455
                                                                                                                                                                                                                                                                                                               LEQYELDEVANWVKAKGQADELVAALDQEQG-KEKPLFDTKKVSRKVTKDGKVGYIMPKD 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVRSDYTGYVTCTTDKLSDKALN------SENPTNLRGNVNLTESANFVLGKA 832
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18.0%; Pred. No. 0.051;
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                                                                                                                                                                                                                                                                                                                                Matches
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEF. 77.
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                                        161 K-----GTKEAKEKGLAQVAHLSKEEVAAVNEAKRQGRYTTDDGYIFSPTD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
642 NHINNERMNGFNGYFGEEEGKNNGNLNVTFKGKSE------QNRFLLTGG-----TN
                                                                                 582 YAFRRIKDGGQLYLNLENYTYYALRKGASTRSELPKNSGESNENWLYMGKTSDEAKRNVM 641
                                                                                                                        123 ----EILDG---YVIKVNGNYYYYLKPGSKRKNI-------RTKQQIAEQVA 160
                                                                                                                                                                   522 LDLNGNSLTFDHIRNIDDGARLVNHNMTNASNITITGESLITDPNTITPYNIDAPDEDNP
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                                                                                                                                                                                                                                                                                     44 DSKGKVKA------PKTNKTMDQISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGK 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Trecartin, Richard REGISTRATION NUMBER: 31,8
                                                                                                                                                                                                         96 ------VPYDAI----
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(415) 398-3240
                                                                                                                                                                                                                                                                                                                                Conservative 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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18.0%; Pred. No. 0.051;
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                                                                               CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA
                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND TITLE OF INVENTION: OF STREPTOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weiser, Jeffrey N. APPLICANT: Plaut, Andrew G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1149 NDPTVNIKEPQSQTNTTADT 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1012 -----SNNEEIARVDEAPVPPPAPAT-----PSETTETVAENSKQESKTVE 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             631 PNVTPLDKRAGMPNWQIIHSAEEVQKALAEGRFAAPDGYIFDPRDVLAKETFVWKDGSFS 690
                                     APPLICATION NUMBER: US/0 FILING DATE: 29-JAN-1997
                                                                                                                                                                                                                                                                    STREET: 1601 Marke
CITY: Philadelphia
STATE: Pennsylvani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 GKDY----FYARYQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAG 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 LEQYELDEVANWVKAKGQADELVAALDQEQG-KEKPLFDTKKVSRKVTKDGKVGYIMPKD 514
                     CLASSIFICATION:
                                                                                                            SOFTWARE:
                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               882 -NVT-----SFYYL--TD 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 KEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGE 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        833 NLFGTIQSRGNSQVRLTENSHWHLTGNSDVH--QLDLANGHIHLNSADNSN------- 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 NAFGYVVPHGD------HYHIIPRSQLSPLEMELADRYLAGQTDDNDSGSDHSKPSD 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 --RDEFKGK---TFKELLDQLHRLDLKYRHVEEDGLIFEPTQVI------KS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 LNGDLTVEKGTLFLSGRPTPHARDIAGISSTKKDPHFAENNEVVVEDDWINR----- 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 IIDDL----GDAYL----VPHGNHYHYI--PKKD--LSPSELAAAQAYWSQKQGRGARPS 254
                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AWKYKLRNVNGRYDLYNPEV-----EKRNQTVDTTNITTPNNIQADVPSVP---- 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KETATVEKEEKAKVETEKTQEV------PKVTSQVSPKQEQSETVQPQAEPARE 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPRADGSSLRTINKSDLSQAEWQQAQELLAKKNAGDATDTDKPEEKQ-----QADKSNE 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NQQPSEASKEEKESDDFIDS 764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSNKQGDKVVVTKSATGNFTLQVADKTGEPNHNELTLFDASKAQRDHLNVSLVGNTVDLG
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                                                                                                                                                                                                                        19103-2398
                                                                                                                                                                                                                                                                Pennsylvania
                                                                                                                                                                                                                                                                                                     E: PANITCH SCHWARZE JACOBS & NADEL, P.C. 1601 Market Street, 36th Floor
                                                                                                       PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                  USA
                                                                                                                                                                      Floppy disk
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                                                             US/08/790,912
                                                                                                                                                                                                                                                                                                                                                                                                   METHODS FOR TREATMENT PNEUMONIAE INFECTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1861 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Leary, Kathryn
                                                                                                                                                                                                                                                                 510 IM------PKDGKDYFYARYQLDL----TQIAFAEQELMLKDKKHYRYDIVDTGIEP 556
                                                                                                                                                                                                                                                                                                                                                         450 YIGFGELEQYELDEVANWVKAKGQADELVAALDQEQGKEKPLFDTKKVSRKVTKDGKVGY 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 HSKPSDKEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGDHFH 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               593 SLD-----AIPSNQENYFVK-----VKSSKFKDVFLPIS------SIVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 EEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELADRYLAGQTDDNDSGSD 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 TPLPEYTGTQSGAIVEPEQVTPSPEYTGVQAGAIVEPEQVASLPEYTGSQAGAIVEPEQV 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 EPPQEYTGNIEPAAPEAENPTEKAQEPKEQKQEPEKNIELRNVSDVELYSLADGKYKQHV 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 TPLPEYTGTQAGAVVSPEQVAPLPEYTGTQSGAIVEPAQVTPLPEYTGVQSGAIVKPAQV 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 IPKKD------LSPSELAAAQAYWSQKQGRGARPSDYRPTP-----APGRRK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 VQSGAIVEPEQVASLPE-----YSGTLSGAIVEPEQIEPEIGGVQSGAIVEPE----QV 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 RIFTVDNAEVSREVLSTKIEEATPKIVEKGTKKLEAPSEKPVTSNLVQPEQVAPLPEYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 PQDEVLSGR--VAKPELLYKETSIETEIAYGEQIQENPDLAEGTVRVKQEGKPGRKIEVV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 PYDAIISEELLMTDPNYHFKQSDVINEILDGYVIKVN-----GNYYVYL--KPGSKRKNI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/026,939 FILING DATE: 23-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 3.0%; Score 131.5; DB Local Similarity 18.1%; Pred, No. 0.091;
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REGISTRATION NUMBER: 36,317
                                        FKGRIVNSYETKAPYNIGGLYGQLTGINALVDKSKATITISSNADSTNQTVGGLAGLVEK 864
                                                                                                                                     SGKTDIGALANEANNAT - - - -
                                                                                                                                                                                RLAVDVSSLPMHAGNATYDTGSSFVIPHIDHIHV------
                                                                                                                                                                                                                      IKGRFTGKLFGSKDGKN--YAIYNLKKPLFDTLSAATVENLTLKD-----VNI 754
                                                                                                                                                                                                                                                                                                                 FYLAKKAER----EVTNFT----SFSNLVQAINNNLNGTYYLAASLNANEVELENGASSY 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NGGYHPAPPRPND----ASQNKHQRDE-FKGKTFKELLD-QLHRL-DLKYR-HV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R-----TKQQIAEQVAKGTKEAKEKGL-------AQVAHLSK--- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EEVAAVNEAKRQGRYT-TDDGYIFSPTDIIDDLG----DAYLVPHGNHYHY 225
                                                                                   ------VPY------SWLTRNQIATIKYVMQHPEVRPDVWSKPGHEES
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--NVTPLDKRAGMPN--WQ------
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                                                                                                                                ----RINNVHVDGVLAGERGIGGLVWKADNSKISNSS
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US-08-296-791-6
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Patent No. 6245337
GENERAL INFORMATION:
APPLICANT: St. Geme III, Joseph W.
APPLICANT: St. Geme III, Joseph W.
APPLICANT: Protein
TITLE OF INVENTION: Haemophilus Adherence and Penetration
TITLE OF INVENTION: Protein
                                                                                                                                                                                                                                                                                                 US-08-296-791-6
                                                                                        В
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TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           865 DALISNSYAEGNINNVKRFGSVAGYLWDRDSSEERHAGRLHNVLSDINVMNGNAISG 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 9411-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,791
FILING DATE: 25-AUG-1994
FILING DATE: 25-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  925 YHYRGMRITDSYSNKDNRVYKVTLEKDEVVTKESLEER-----GTILDVSQIASKKSEI- 978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     785 KANIDPKYLIFQPEGVQFYNKNGELVTYDIKTLQQIN 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           730 TDK----PEEKQQADKSNENQQPSEASKEEKESDDFIDSLPDYGLDR--ATLEDHINQLAQ 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          979 --NSLSAPKVETLLTSTNKESDESKVKDYQASRALAYKNIEKLLPFYNKATIVKYGNLVK 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    685 KDGSFSIPRADGSSLRTINKSDLSQAEWQQAQELLAKKNA-------GDATD 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-59941/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
545 IRNIDDGARVVNHNMTNTSNITITGESLITNPNTITSYNIEAQD-----DDHPLRIRSI 598
                                            101 I-----ISEELLMTDPN----YHFKQSDVINEILDGYVIKV--- 132
                                                                                        487 KQKADANNKV--QAFSQVGIVSGRSTLVLNDDKQVDPNSIYFGFRGGRLDLNGNSLTFDH 544
                                                                                                                                                                                                                                                                                                                   LENGTH: 1848 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                y Match 3.0%; Score 130.5; DB 4; Length 1848; Local Similarity 17.2%; Pred. No. 0.11; hes 159; Conservative 120; Mismatches 327; Indels 319; Gaps
                                                                                                                                    48 KVKAPKTNKTMDQISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGK------VPYDA 100
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RESU PCT Se	Qу	Qy Db	Qу	Qу	Qу	Qy Db	Qу Дъ	Qy Db	Qу	Db Qy	P 24	OD VY	ob VY	צי ע
SULT 12 Sequence 6, Application PC/TUS9510661A Sequence 6, Application PC/TUS9510661A Sequence 6, Application PC/TUS9510661A Sequence 6, Application Protein Information: University, et al. APPLICANT: Washington University, et al. TITLE OF INVENTION: Haemophilus Adherence and Penetration Protein NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: 9 CORRESPONDENCE ADDRESS: Plehr, Hohbach, Test, Albritton & Herbert ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco COUNTRY: United States ZIP: 94111-4187 COMPUTER READABLE FORM:	798 EGVQEYNKNGELVTYDIKTLOQINP 822 : :	753 KEEKESDDFIDSLPDYGLDRATLEDHINGLAQKANID	11	: : KVA 11	10	EVRP 61 NGRY 99	SSLP 5 SA 9	00	4 6	327 RHVEEDGLIFEPTQVIKSNAFGVVVPHGDHYHIIPRSOLSPLEMELADRYLAGQTDDNDS 386	267 APIPDVTPNPGQGHQPDNGGYHPAPPRPNDASQNKHQRDEFKGKTFKELLDQLHKLULKI 320	GRRK 26 - -NFK 75	NVEKGTL	KGTKEAK 16

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REFERENCE/DOCKET NUMBER: FP-5(
TELLECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277799
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1848 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 159;
567 MHAGNATYDTGSSEVIPHIDHIHVVPYSWLTRNQIATI------KYVMQHPEVRP 615
                                           905 -----KVVVNKSA-- 932
                                                                                 507 VGYIMPKDGKDYFYARYQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPRLAVDVSSLP 566
                                                                                                                          865 HWHLTGNSNVNQLNLTNGHTHLNAQNDANKVTT------YNTLTVN------ 904
                                                                                                                                                                   447 HFHYIGFGELEQYELDEVANWVKAKGQADELVAALDQEQGKEKPLFDTKKVSRKVTKDGK 506
                                                                                                                                                                                                                                                        387 GSDHSKPSDKEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGD 446
                                                                                                                                                                                                                                                                                                   787 VHI---GYKTGDTVCVRSDYTGYVTCHNSNLSEKALNSENPTN-----LRGNVNLTEN 836
                                                                                                                                                                                                                                                                                                                                          327 RHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHIIPRSQLSPLEMELADRYLAGQTDDNDS 386
                                                                                                                                                                                                                                                                                                                                                                                       755 ATTMNVTGNASL-----------YSGRNVANITSNITASNNAQ 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 EKGLAQVAHLSKEEVAAVNEAK------RQGRYTTDDGYIFSPTDIIDDL----GDA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           599 PYRQLYFNQDNRSYYTLKKGASTRSELPQNSGESNENWLYMGRTSDAAKRNVMNHINNER 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 ------RTKQQIAEQVAKGTKEAK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487 KOKADANNKV--QAFSQVGIVSGRSTLVLNDDKQVDPNSIYFGFRGGRLDLNGNSLTFDH 544
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ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10661A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 KVKAPKTNKTMDQISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGK------VPYDA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 watch 3.0%; Score 130.5; DB 5; Length 1848; Local Similarity 17.2%; Pred. No. 0.11; Local Similarity 17.2%; Mismatches 327; Indels 319; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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GRADUS-08-663-112-2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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Patent No. 5849503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                   y Match
J.0%; Score 130; DB 2; Length 765;
Local Similarity 19.2%; Pred. No. 0.03;
hes 155; Conservative 107; Mismatches 264; Indels 280; Gaps
86 GDHYHFYNGKVPYDAIISEELLMTDPNYH-FKQSDVINEILDGYVIKVNGNYYVYLKPGS 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KURITA, NO. 58495031ko
TITLE OF INVENTION: MUTANT PROTEINS OF HUMAN DNA
TITLE OF INVENTION: TOPOISOMERASE I
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                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                          TELEPHONE: ZUZ ... TO NO:
                                                                                                                                                                                                                                                                                                                                                NAME: Elnaudi, Carolyn P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1103 ENPPOENETVAKNEQEATEPTPQNGEVAKEDQPTVEANTQTNEATQSEGKTEETQTAETK 1162
                                                                                                                                                                                                                             TYPE:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                       amino acid
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IBM PC compatible
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3 GDHLH------HKKEKDRELNDSHKHKDKHKDREHRHKE-----HKKEKDRE 45

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590 RTFNASTTLQ---QULKELTA-------PDENIPAKILSYNRANRAVAILCNHQR 634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548 FKNLQLEMENKQ------PEDDLEDRLNTGILNKHLQDLMEG-----LTAKVF 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                642 MPNWQIIHSABEVQKALAEGRFAAPDGYIFDPRD--VLAKETFVWKDGSFSIPRADGSSL 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 587 ----HIHVVPYSWLTRNQIATIKYVMQHPEVRPDVWSKPGHEESGSVIPNVTPLDKRAG 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 KIRNQYREDWKSKEMKVRQRAVALYFIDKLALRAGNEKEEGETADTVGCCSLRVEHINLH 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 HDNKVTWLVSWTENIQGSIKYIMLNPSSRIKGEKDWQKYETAR------RLKKCVD 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498 -SRKVT------KDGKVGYIM------PKDGKDYFYARYQLDLTQIAFAEQELML 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383 DNDSGSDHSKPSDKEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESI--HSVDKSGV 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 SNAFGYVVPH-----------GDHYHIIPRSQLSPLEMELADRYLAGQTD 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 ATFFAKMLDHEYTTKEIFRKNEFKDWRKEMTNEEKNII--TNLSKCDFTOMSQYFKAQTE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 EQKWKWWEE---ERYPEGIKWKFLEHKGPVFAPPYEPLPENVKFYYDGKVMKLSPKAEEV 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 EFKGKTFKELLDQLHRLDLKYRHVEEDGLIFEPT------QVIK------ 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 KEKENGF-SSPPQIKDEPEDDGYFVP-----PKEDIKP-----LKRPRDED 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 KRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSK------EEVAAVNEAKRQGR 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1181 amino acids
598 RNQIATIKYVMQHPE-----VRPDVWSKPGHE-----ESGSVIPNVTPLDKRAGM 642
                                        691 RDLYD------PRDKAKLLYN------NLDAFGIMDYT-LTGKVEDNHDD 727
                                                                                 547 YDIVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPHIDHIHVVPYSWLT------ 597
                                                                                                                         638 SEKY-----YVLKKGEKDYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLTASERNLDF 690
                                                                                                                                                                  498 SRKVTKDGKVGYIMPKDGKDY------FYARY-QLDLTQIAFAEQELMLKDKKHYR 546
                                                                                                                                                                                                        590 IVT-HDNDIFRTI-----LPMDQEFTYRVKNREQA----YRINKKSGLNEEINNTDLI 637
                                                                                                                                                                                                                                                   439 GVTAKHGDHFHYIGFGELEQYELDEVANW-VKAKGQADELVAALDQEQGKEKPLFDTKKV 497
                                                                                                                                                                                                                                                                                           542 ----FRPGLKDTKLLKTLAIGDTITSQELLAQAQSILNKNH---PGY-----TIYERDSS 589
                                                                                                                                                                                                                                                                                                                                    387 GSDHSKPSDKE------VTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKS 438
                                                                                                                                                                                                                                                                                                                                                                             487 ADKDGSVTLPTQPVQEFLLSGHV----RVRYKEKPIQNQAKSVDVEYTVQFTPLNPDDD-- 541
                                                                                                                                                                                                                                                                                                                                                                                                                     329 VEEDGLIFEPTQVIKSNAF-GYVVPHGDHYHIIP-RSQLSPLEMELADRYLAGQTDDNDS 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                              429 KPFATDSGAMSHKLE--KADLLKAIQEQLIANVHSNDDYFEVIDFASDATITDRNGKVYF 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 PPRPNDASONKHORDEFKGKTFKELLDOL----HRLD------LKYRH 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 -----IEGRNNSQLVVSVAGTVEGTNQDISLKFFEIDLTSRPAHGGKTEQGLSPKS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 RPSDYRPTPAPGRRKAPIP------290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 GRYTTDDGYIFSPTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQAYWSQKQGRGA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 GRQTVDEA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 KDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAA--S 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 KRKNIR--TKQQIAEQVAK-----GTKEAKEKG--LAQVAHLS----KEEVAAVNEAKRQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 -----PFVGVLSAGINAASPN-----KELAKEFLENYLLTDEG-----LEAVN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 HMN-ADTDYSTAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVT-----VLPTFKGQPSK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 HGDHYHEYNGKVPYDAIISEELLMTDPNYHFKQSDVINEILDGYVIKVNGNYYVYLKPGS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 HMGLATKDNQIAYIDDSKGK----VKAPKTNKTMDQISAEEGISAEQIVVKITDQGYVTS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 3.0%; Score 129; DB 2; Length 1181; Local Similarity 18.8%; Pred. No. 0.071;
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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US-08-488-940-2 Sequence 2, Application US/08488940 Patent No. 5854049

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PLA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

COUNTRY: USA ZIP: 02110-2804

STATE:

Boston MA

225 Franklin Street Fish & Richardson P.C

STREET:

ADDRESSEE:

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516 PELDGQEYVVEFDFLGKD---SIRYY-----

Qy	Дb	Qy	Db Qy	Qy Db	Qy Db	g Qy	Фр	Qy Db	Db 5	Que Bes Mat	RESULT 523116 ;Paten ;Vuust vuust T ; T ; SEQ 1 ;SEQ 1	0y 0y 0y 0y 0y	Db Qy
465 ANWVKAKGQADELVAALDQEQGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGKDYFYARYQ 524 ; :: : : : : : : : : : : : : :	REDDKSAHIQHEIVEV 38	IHSVDKSGVTAKHGDHFHYIGFGELEQYELDEV 46	1 A 34	HVEEDGLIFEPTQVIKSNAFGYVVEHG	GYHPAPPRENDAS : VDSQPNPQEPVEPSFVKIEK 26	SEKSTSEPAEHVESVSEQ 20	AAVNEAKRQGKYTTUUGIIESETU NEEGDFEEPNHEEFEPDQ	NGNII VILAFGUAN ESNPEPAENEESSI	::: :: :: :: :: ::	2.9%; Score 127.5; DB 6; Length 783; sery Match 18.3%; Pred. No. 0.049; st Local Similarity 18.3%; Pred. No. 0.049; (tches 159; Conservative 137; Mismatches 294; Indels 281; Gaps 42; (tches 159; Conservative 137; Mismatches 294; Indels 281; Gaps 42;	RESULT 15 5231168-2 FATENT NO. 5231168 ; PATENT NO. 5231168 ; PATENT NO. 5231168 ; PATENT NO. 5231168 ; PUUST, JENS; RIENECK, KLAUS, WIND, ANNETTE; JAKOBSEN, PALLE H. TITLE OF INVENTION: MALARIA ANTIGEN NUMBER OF SEQUENCES: 19 ; CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/409,658 FILING DATE: 18-SEP-1989 ; SEQ ID NO:2: LENGTH: 783	SY SSLRTINKSDLSC:	: : : :

рь	Qy	дb	Qy	Db	Qy	ДĎ	Οy	Db	Qy	DЬ	Qy	DЬ
659	795	628	735	568	697	511	642	462	583	420	525	387
PSEGESTKPDIVQIKIVQENKP 680	795 FQPEGVQFYNKNGELVTVDIKTLQQINP 822	EKK	EKQQADKSNENQQPSEASKEEKESDDFIDSLPDYGLDRATLEDHINQLAQKANIDPKYLL /94			NEKVQHEIVEVEEILPEDKNEKGQHEIVEVEEILPEEDKNEK-GQHEIVEVEELLEED	642 MPNWQIIHSABEVQKALAEGREAAPDGYIEDPRDVLAKETFVWKDGSE'SIPKADG	VEVEEI LPEDKNEKVEHEIVEVEEILPEDKNEKGUHEIVEV EELLEUV.	583 PHIDHIHVVPYSWLTRNOIATIKY-VMOHPEVRPDVWSKPGHEESGSV1PWYTELDARMS	HEIVEVEEILPEDDKNEKVEHEIVEVEEILFEDONENGKIID	525 LDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPRLAVDVSSLPMHAGNATTUIGSSEY 1 502 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	387EEILDEDDKNEKVEHEIVEVEEILPEDKNEKQQ 419

Search completed: December 3, 2001, 07:16:20 Job time: 149 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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:/cgn2_6/ptcdata/2/paa/USO80_COMB.pep:*
:/cgn2_6/ptcdata/2/paa/USO81_COMB.pep:*
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:/cgn2_6/ptcdata/2/paa/USO83_COMB.pep:*
:/cgn2_6/ptcdata/2/paa/USO83_COMB.pep:*
:/cgn2_6/ptcdata/2/paa/USO85_COMB.pep:*
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1 VKKTYGYIGSVAAILLATHI.....YNKNGELVTYDIKTLQQINP 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
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SUMMARIES
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Result		Query Match Length DB	ength	DВ	ID	Description
1	4363	100.0	822	- ;	PCT-US00-23417-6	Sequence 6 Appli
۵	4363	100.0	822	20	US-09-645-835-6	Sequence 6. Appli
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4	4312.5	98.8	824	18	US-09-471-255-83	Sequence 83 April
u	4308	98.7	823	18	US-09-471-255-81	Secuence 81 Appl
0	4283.5	98.2	825	_	PCT-US00-23417-2	Sequence of Appli
7	4283.5	98.2	825	20	US-09-645-835-2	Tradity (# 0000000
8	4283.5	98.2	825	20	US-09-645-835A-2	Sequence 2 Appli
9	4157	95.3	793	16	US-09-252-088-15	Sequence 15, Appl

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9-765-27	-09-536-784-56	-09-583-110-3	-09-468-656-	-09-645-8352	-09-471-255	-09-471-255	9-471-255	9-583-110	-09-471-255	-09-471-255	-09-471-255	-09-765-272	09-765-271	-09-536-784	-09-471-255	9-471-255	-09-471-255	-09-468-656-4	S-09-471-255	S-09-787-826	S-09-283-094	S-09-471-255	S-09-471-255	S-09-471-255	S-09-471-255-96	S-09-58	S-09-471-255-14	S-09-471-255-101	S-09-107-433	-09-471-255	-09-471-255	S-09-468-656	-09-252-088	88-16	-09-252-088
equenc	equence 56.	equence 3851,	equence 8, A	equence 7, A	equence 79,	equence 102, Ap	equence 60, App	equence 385	equence 4, Appl	equence 91, App	equence 94,	equence 66,	Sequence 66, Appl	equence 66	equence 90, App	equence 73, App	equence 97, App	4	100,	J .	57	9 1	2	98	96.	Sequence 5225, Ap	equence 14.	equence 101	equence 4309. A	equence 95, App	uence 99, Ap	equence 10, Ap	uence 16, Ap	equenc	5, Ap

ALIGNMENTS

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                                                                                                                                                                ; LENGTH: 822
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
PCT-US00-23417-6
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                                                                       Ouery Match 100.0%; Score 4363; Best Local Similarity 100.0%; Pred. No. 0; Matches 822; Conservative 0; Mismatches
                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 6
                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
1 VKKTYGYIGSVAAILLATHIGSYQLGKHHMGLATKDNQIAYIDDSKGKVKAPKTNKTMDQ 60
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US00/23417
FILING DATE: 2000-08-25
PLICATION NUMBER: U.S. 60/150,750
LING DATE: 1999-08-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    T: Johnson, Leslie S.
T: Koenig, Scott
F: Adamou, John E.
INVENTION: Pneumococcal Protein Homologs and Fragments for INVENTION: Vaccines
                                                                                                                                                                                                                                                     PatentIn Ver. 2.1
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                                                                                                                                           APPLICANT: Heinrichs, Jon
APPLICANT: Johnson, Leslie S.
APPLICANT: Koenig, Scott
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Pneumococc
TITLE OF INVENTION: Vaccines
FILE REFERENCE: 469201-402
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09645835
                               SEQ ID NO 6
                                                                         CURRENT APPLICATION NUMBER: US/09/645,835
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: U.S. 60/150,750
PRIOR FILING DATE: 1999-08-25
                                                SOFTWARE:
                                                              NUMBER OF SEQ ID NOS:
TYPE: PRT
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US-09-645-835A-6
; Sequence 6, Application US/09645835A
; GENERAL INFORMATION:

APPLICANT: Heinrichs, APPLICANT: Johnson, I APPLICANT: Koenig, St APPLICANT: Adamou, Jo

Leslie

Adamou, John E Koenig, Scott

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PRIOR APPLICATION NUMBER: U.S. 60/150,750
PRIOR FILING DATE: 1999-08-25
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APPLICANT: BRODEUR, Bernard R.
APPLICANT: APPLICANT: DINEAU, Isabelle
APPLICANT: RIOUX, Cl.ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113,800
PRIOR APPLICATION NUMBER: US 50/113,800
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 83
LENGTH: 824
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Best Local S
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APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: RIOUX, Cl.ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
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APPLICANT: HAMEL, Jos,e
APPLICANT: BRODEUR, Bernard R
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
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CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113,800
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 102
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                                                                                   KHQRDEFKGKTFKELLDQLHRLDLKYRHVEEDGLIFEPTQVIKSNAFGYVVPHGDHYHII
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PRIOR FILING DATE: 1999-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 2
LENGTH: 825
TYPE: PRT
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PCT-US00-23417-2
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Best Local :
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APPLICANT: Johnson, Le
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                                                                                                                                                     ISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYHFKQSDV 120
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                                EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQ 240
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EVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAAQ
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1999-08-25
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                                                        Query Match
Best Local S
Matches 810
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GEMERAL INFORMATION:
APPLICANT: Heinrichs, Jon
APPLICANT: Johnson, Leslie S.
APPLICANT: Koenig, Scott
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Pneumococcal Protein Homologs and
TITLE OF INVENTION: Vaccines
FILE REFERENCE: 469201-402
                                                                                                                                                                    SEQ ID NO 2
LENGTH: 825
                                                                                                                            TYPE: PRT
ORGANISM: Streptococcus
-09-645-835-2
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/645,835
CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: U.S. 60/150,750
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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1 VKKTYGYIGSVAAILLATHIGSYQLGKHHMGLATKDNQIAYIDDSKGKVKAPKTNKTMDQ 60
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                                                       Score 4283.5;
Pred. No. 0;
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RESULT 8
US-09-645-835A-2
Sequence 2, Application US/09645835A
GENERAL INFORMATION:
APPLICANT: Heinrichs, Jon
APPLICANT: Johnson, Leslie S.
APPLICANT: Koenig, Scott
APPLICANT: Adamou, John E.
TITLE OF INVENTION: Pneumococcal Protein Homologs and
TITLE OF INVENTION: Vaccines
FILE REFERENCE: 469201-493
CURRENT APPLICATION NUMBER: US/09/645,835A
CURRENT APPLICATION NUMBER: US. 60/150,750
PRIOR APPLICATION DATE: 2000-08-25
PRIOR APPLICATION NUMBER: US. 60/150,750
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEO ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 825
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RESULT 9
US-09-252-088-15
; Sequence 15, Application US/09252088
; GENERAL INFORMATION:
   APPLICANT: BRODEUR, Bernard R.
   APPLICANT: BOYER, Martine
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ORGANISM: Str
S-09-645-835A-2
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Best Local Similarity
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Pred. No. 0;
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APPLICANT: HAMEL, Jose
APPLICANT: HAMEL, Jose
APPLICANT: HAMEL, Jose
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOC
FILE REFERENCE: 8331-9002
CURRENT APPLICATION UNMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 793
TYPE: PRT
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   EASKEEKESDDFIDSLPDYGLDRATLEDHINQLAQKANIDPKYLIFQPEGVQFYNKNGEL
                EASKEEKESDDFIDSLPDYGLDRATLEDHINQLAQKANIDPKYLIFQPEGVQFYNKNGEL
                                                       {\tt SIPRADGSSLRTINKSDLSQAEWQQAQELLAKKNTGDATDTDKPKEKQQADKSNENQQPS}
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APPLICANT: BRODEUR, Bernard R.

APPLICANT: RIOUX, Clement
APPLICANT: ROVER, Martine
APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: HAMEL, Josee
APPLICANT: HAMEL, Josee
APPLICANT: HAMEL, Josee
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANT
FILE REFERENCE: B331-9002
CURRENT APPLICATION UNMBER: US/09/252,088B
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/60/075,425
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 45
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US-09-252-088B-15
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SEQ ID NO 15
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Best Local Similarity
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                                                                                                           HSKPSDKEVTHTFLGHRIKAYGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGDHFH 449
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                                                                                                                                                                                                                                                                      EEDGL1FEPTQV1KSNAFGYVVPHGDHYH11PRSQLSPLEMELADRYLAGQTDDNDSGSD
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                                               MMPKDGKDYFYARDQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPRLAVDVSSLPMHA
                                                                IMPKDGKDYFYARYQLDLTQIAFAEQELMLKDKKHYRYDIVDTGIEPRLAVDVSSLPMHA
                                                                                                                                                                                                                                       EEDGL1FEPTQV1KSNAFGYVVPHGDHYH11PRSQLSPLEMELADRYLAGQTEDNDSGSE
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Pred. No. 0;
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GENERAL INFORMATION:
APPLICANT: BRODEUR, Bernar
APPLICANT: RIOUX, Clment
APPLICANT: BOYER, Martine
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SEQ ID NO 16
LENGTH: 715
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Best Local Similarity 98.5%;
Matches 704; Conservative
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CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
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APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
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                                       KAYGKGLDGKPYDTSDAYVFSKESIHSVDKSGVTAKHGDHFHYIGFGELEQYELDEVANW 467
                                                                                                                                           GYVVPHGDHYHIIPRSQLSPLEMELADRYLAGQTDDNDSGSDHSKPSDKEVTHTFLGHRI 407
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  VKAKGQADELVAALDQEQGKEKPLFDTKKVSRKVTKDGKVGYIMPKDGKDYFYARYQLDL
                                                                                                                      GYVVPHGDHYHIIPRSQLSPLEMELADRYLAGQTEDNDSGSEHSKPSDKEVTHTFLGHRI
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Pred. No. 2.9e-299;
6; Mismatches 5;
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SEQ ID NO 16
LENGTH: 715
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ORGANISM: group B streptococcus
-09-252-088B-16
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/60/075,425
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 45
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TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
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APPLICANT: RIOUX, Cl
APPLICANT: BOYER, Ma
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APPLICANT:
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GYVVPHGDHYHIIPRSQLSPLEMELADRYLAGGTDDNDSGSDHSKPSDKEVTHTFLGHRI 407
                                                                                                HPAPPRPNDASQNKHQRDEFKGKTFKELLDQLHRLDLKYRHVEEDGLIFEPTQVIKSNAF 347
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BOYER, Martine
CHARLEBOIS, Isabelle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09468656 GENERAL INFORMATION:
APPLICANT: Johnson, Leslie S.
                                                                                                                                                                                                                                                                                                                                                     Matches 295;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Streptococcus Pneumoniae and TITLE OF INVENTION: Vaccines FILE REFERENCE: 469201-44
CURRENT APPLICATION NUMBER: US/09/468,656
CURRENT FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/113,048 EARLIER FILING DATE: 1998-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Koenig, Scott
APPLICANT: Adamou, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 819
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                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                             1 VKKTYGYIGSVAAILLATHIGSYQLGKHHMGLATKD-NQIAYIDDSKGKVKAPKTNKTMD
                                                                                                                                                                                                              QISAEEGISAEQIVVKITDQGYVTSHGDHYHFYNGKVPYDAIISEELLMTDPNYHFKQSD 119
QAYWSQKQGRGARPSDYRPTPAPGRRKAPIPDVTPNPGQGHQPDNGGYHPAPPRPNDASQ 299
                                      EEVAAVNEAKRQGRYTTDDGYIFSPTDIIDDLGDAYLVPHGNHYHYIPKKDLSPSELAAA 239
                                                                                                                  IVNEIKGGYVIKVNGKYYVYLKDAAHADNIRTKEEIKRQ-----KQERSHN-----HNSR 167
                                                                                                                                                      VINEILDGYVIKVNGNYYVYLKPGSKRKNIRTKQQIAEQVAKGTKEAKEKGLAQVAHLSK 179
                                                                                                                                                                                            EVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYQLKDSD
                                                                                                                                                                                                                                                                       INKKY-LAGSVA--VLALSVCSYELGRYQAGQDKKESNRVAYIDGDQAGQKA--ENLTPD
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                                                                                                                                                                                                                                                                                                                                                   Conservative 103; Mismatches 235;
                                                                                                                                                                                                                                                                                                                                                                     24.2%;
                                                                                                                                                                                                                                                                                                                                                                   Score 1054; DB 18; Pred. No. 7.9e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic
                                                                                                                                                                                                                                                                                                                                               Indels 246; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Length 819;
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APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, Jos, e
APPLICANT: HRODEUR, Bernard R.
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: MARTIN, Denis
APPLICANT: RIOUX, Cl.ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
                                                                                                                    ; ORGANISM: S. pneumoniae US-09-471-255-99
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                      Matches
                                                                                                                                                                                                         SEQ ID NO 99
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GENERAL INFORMATION:
                                                                                                                                                                                                                  CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113,800
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 102
SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                   LENGTH: 811
                    Watch 24.18; Score 1052; DB 18; Length 811; Local Similarity 36.18; Pred No. 1.1e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703 NKSDLSQAEWQQAQELLAKKNAGDATDTDKPEEKQQADKSNENQQPSEA--SKEEKESDD 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 PNAQITYTDDEIQVAKLAGKYTAEDGYIFDPRDITSDE-----GDAYVTPHMTHS--HWI 560
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             Conservative
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      88; Mismatches 212;
  Indels 178;
Gaps
26;
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APPLICANT: BIOCHEM PHARMA INC.
APPLICANT: HAMEL, Jos,e
APPLICANT: BRODEUR, Bernard R.
APPLICANT: BRODEUR, Bernard R.
APPLICANT: PINEAU, Isabelle
APPLICANT: MARTIN, Denis
APPLICANT: RIOUX, C1,ment
TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 12806-11PCT
CURRENT APPLICATION NUMBER: US/09/471,255
CURRENT FILING DATE: 1999-12-23
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NUMBER OF SEQ ID NOS: 102
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 95
LENGTH: 834
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                                                                                  PRIOR APPLICATION NUMBER: US 60/113,800 PRIOR FILING DATE: 1998-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 HYRYDIVDTGIEPRLAVDVSSLPMHAGNATYDTGSSFVIPHIDHIHVVPYSWLTRNQIAT 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 ---LVKEAVRKV------GDGY------VFEENGVPRYIPAKDLSAETAAGIDS 404
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; TYPE: PRT; ORGANISM: S. pneumoniae US-09-471-255-95
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Search completed: December 3, 2001, 07:22:36 Job time: 525 sec
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                                                                                                                                                                                                                                                                                        452 QVDFEALDNLLE-RLK-DVSS-------DKVKLV------DDTLA 481
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                                                                                                                                                   516 TTEDGYIFDPRDITSDE-----GDAYVTPHMTHS--HWIKKDSLSEAERAAAQAYAKEKG 568
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                                                                                                                                                                                                                       482 FLAPIRHPE---------RIGKPNAQTTYTDDEIQVAKLAGKY 515
                                                                                   569 L-----TPPSTDHQDSGNTEAKGAEA 589
                                                                                                                  724 AGDATDTDKPEEKQQADKSNENQQPSEA 751
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Result
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Perfect score:
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       US-08-081-929-2
5268270-2
US-08-042-846-2
PCT-US93-03077-1
US-08-471-043-50
US-08-471-046A-50
US-08-471-046A-50
US-08-470-566B-50
US-08-470-568B-50
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Sequence 66, Appl
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Sequence 4, Appli			Sequence 2, Appli	Sequence 1, Appli	ω.	Sequence 17, Appl	Sequence 37, Appl	37					Sequence 48, Appl	42		2	Sequence 8, Appli

ALIGNMENTS

; TOPOLOGY: linear; ; MOLECULE TYPE: protein US-08-961-083-56 US-08-961-083-56 Query Match Best Local Similarity Matches 795; Conserv Sequence 56, Application US/08961083 Patent No. 6159469 GENERAL INFORMATION: TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50: COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS Vers: SOFTWARE: ASCII Text CURRENT APPLICATION DATA: REFERENCE/DOCKET NUMBER: PB. TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders PRIOR APPLICATION DATA: APPLICATION NUMBER: APPLICANT: Choi et. TITLE OF INVENTION: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: APPLICANT: TYPE: amino acid STRANDEDNESS: sir STREET: 9410 Key CITY: Rockville STATE: Maryland NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, FILING DATE: CLASSIFICATION: 435 FILING DATE: APPLICATION NUMBER: LENGTH: COUNTRY: ADDRESSEE: 20850 796 amino acids 9410 Key West Avenue USA Human Genome Sciences, Inc. Diskette, 3.50 inch, 1.4Mb storage single 97.6%; 99.9%; al. Streptococcus pneumoniae Antigens and Vaccines 452 MSDOS version 6.2 US/08/961,083 36,373 PB340P2

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21 SYELGLYQARTVKENNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYYT

Conservative

0; Mismatches Score 4163; DB Pred. No. 0;

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Length 796; Indels

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; Patent No. 6159469
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                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                  STREET: 9410
CITY: Rockville
CTATE: Maryland
               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                             781 LLKGSNPSSVSKEKIN 796
                                                 COUNTRY: U
ZIP: 20850
COMPUTER: HP Vectra 486/33
                                                                                                                                ADDRESSEE:
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LENGTH: 763 amino acids
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REFERENCE/DOCKET NUMBER:
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GAEAIYNRVKAAKKVPLDRMPYNLQYTVEVKNGSLIIPHYDHYHNIKFEWFDEGLYEAPK 645
                                    SAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIKFAWFDDHTYKAPN 674
                                                                                                HDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANPTGD 614
                                                                                                                                                                                                                                                                                                                                                                                     RTARGVAVPHGNHYHFIPYEQMSELEKRIARIIPLRYRSNHWVPDSRPEQPSPQSTPEPS
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                                                                            RDITSDEGDAYYTPHMTHSHWIKKDSLSEAERAAAQAYAKEKGLTPPSTDHQDSGNTEAK 585
                                                                                                                                                      KDVXSDKVKLVXDILAFLAPIRHPERLGKPNAQITYTDDEIQVAKLAGKYTTEDGYIFDP 525
                                                                                                                                                                                        NDESTNKEKLYDDLLAFLAPITHPERLGKPNSQIEYTEDEVRIAQLADKYTTSDGYIFDE 554
                                                                                                                                                                                                                                                                         LSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEAHKALFENKGRNSDFQALDKLLERL
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энGG I I	RTKD:	RTKE	NAAH		YQAR ::::	Simi 3;		-182	GY:	EDNE	CH	Ż	NO	NCE,	RAT	AG:	ATIO	PLIC	DA	APP	RE:	TER:	RE	20850	: ::		SSEE	S FO	I N	NEOE 15	3-18	EETI	PVEET-	TLE	TLE
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RESULT 4
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;Patent No. 5231168
;VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.
TITLE OF INVENTION: MARAIARIA ANTIGEN
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/409,658
FILING DATE: 18-SEP-1989
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305 IPVNEDEFEDVHTEQLDLDHKTVDPEIVEVEEIPSELHENEVAHPEIVEIEEVFPEPNQN 364
                                           452 VAPRDQEFYDKAYNLLTEAHKA------LFENKGRNSDFQALDKLLERLNDE 497
                                                                                      245 PNFVDSQPNPQEPVEPSFVKIEKVPSEENKHASVDPEVKEKENVSEVVEEKQNSQESVEE 304
                                                                                                                                 405 EGYVF-----EEKGISRYVFAKDLPSETVK--NLESKLSKQESVSHTLTAKK-----EN 451
                                                                                                                                                                                 190 SEKSTSE---PAEHVESVSEQSNNEPSEKKDGPVPSKPFEEIEKVDVQPKIVD--LQIIE 244
                                                                                                                                                                                                                       352 PLRYRSNHWVPDSRPEQPSPQPTPEPS---PGPQPAPNL----KIDSNSSLVSQLVRKVG 404
                                                                                                                                                                                                                                                                       132 EGDFEEPNHEEFEPDQNDSELSENELVESEKSVSEP-AEHVEIVSEKSVSEPAEHV-EIV 189
                                                                                                                                                                                                                                                                                                                  311 ------FDPAQITS------RTARGVAVPHGDHYHFIPYSOMSELEERIARII 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 EDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRTYRRQ--NSDNTSRT 255
                                                                                                                                                                                                                                                                                                                                                                                                      256 NWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLYKLPLSQRHVES--DGLV--- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 ----SVTEPAEHEEVVSEESNPEPAENEESSIEEAHQE--EIVPEQNDEESGESGLVDNE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                      35. EESGESKLV------DNDEGGFEEAHHENFSS---EVSNSELNENEFVESDK---- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 AAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYH 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 AYIVRHGDHFHYI-----PKSNQIGQPTLPNNSLATPSPSLPI--NPGTSHEKHEEDGY 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 AYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSPDADVKANP-----TGDSA 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 -----SDGYIFNPKDIVEETAT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 ----ISGTGSTVSTNAK----- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 -LTTSKE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 APNLKIDSNSSLVSQLVRKVGEGYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSH 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 PGTTNINTSNASNINSOASOSNDIDSLLKOLYKLPLSOGHVESDGLVFDPAQITSRTARG 323
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SEQ ID NO 6
LENGTH: 1073
TYPE: PRT
ORGANISM: S.pombe
US-09-541-782-6
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APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 6, Application US/09541782
Patent No. 6284480
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEO ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 EIVEVE---EILPE------DDKNEKVEHEIVEVEEILP--EDKNEKGQHEIVE 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 NEFQEINEDDKSAHIQHEIVEVEEILPEDDKNEKVEHEIVEVEEILPEDKNEKG----QH 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 498 STNKEKLVDDLLAFLA-PITHPERLGKPNSQIEYTEDE-VRIAQLADKYTTSDGYIFDEH 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         777 LRNNLTLQIMDNNSIMAEAEKLLALLKGSNPSSVSKEKI 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 LPEDKNEKVQHEIVE----VEEILPEDKNEKVQHEIVEVEEILPEIVE-----IEEVPSQ 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 EILPEDKNEKVQHEIVEVEEILPEDKNEKGQHEIVEVEEILPEEDKNEKGQHEIVEVEEI 563
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                                                                                                                                                                                                                                                             146 VRTKEEINRQKQEHS-----QHREGGTPRNDGAVALARSQGRYTTDDGYIFNASDIIEDT 200
                                                                                                                                                                                                                                                                                                                                                                          147 GQTGTGKTYTMSGD-LSDSDGILSEGAGLIPRALYQLFSSLDNSNQEYAVK-CSYYELYN 204
407 K---SIRNKPQNNQLVFRKVLIKDLVLDIERLKNDLNATRKKNGVYLAESTYKELMDRVQ 463
                                                                       350 NALVEKAHHIPYRESKLTRLLQDSLGGKTKTSMIVTVS---STNTNLEETISTLEYAARA 406
                                                                                                            244 -----YR-----RONSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSOASQS 284
                                                                                                                                                                                      201 GDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGNLSNSRT---------
                                                                                                                                                                                                                           261 VAATKCNDLSSRSHSIFTITLHRKVSSGMTDETNSLTINN------NSDDLLR--
                                                                                                                                                                                                                                                                                                   205 EEI-RDLLVSEEL--RKPARVFEDTSRRGNVVITGIEESY-IKNAGDGLRLLREGSHRRQ 260
                                                                                                                                                                                                                                                                                                                                                                                                              43 GKQATQKTENLTPDEVSKREGINAE------QIVIKI--TDQGYVTSHGDHYHYYN 90
                                                                                                                                                                                                                                                                                                                                    91 GKVPYDAIISEELLMKDPNYKLKDED-----IVNEVKGGYVIKVDGKYYVYLKDAAHADN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYTLEDLFATIKYYVEHPDE-RPHSNDGWGNAS----EHYLGKKDHSE------ 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DPNKNFKADEEPVEETPAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSLKANATETLAG 776
                                                                                                                                                  -----ASKLHMVDLAGSENI--GRSGAENKRARETGMINQSLLTLGRVI 349
                                   NDIDSLLKQLYKLPLSQRHVESDGLVFDPAQI----TSRTARGVAVPHGDHYHFIPYSQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                       182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.4%; Score 145.5; DB 18.6%; Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 1073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             357; Indels 301; Gaps
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                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                 FILING DATE:
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                                                                                                                                                                                                                                                                 USA
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Sequence 118, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 NKDLLCQEQARKLEVLDLNVKS-----SREQLQYVSKSNQEHKKEVEALQLQLVNSSTE 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 LTAKKENVAPRDQEFYDKAYNLL-----TEAH 471
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                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     517 -HPERLGKPNS-----VR--IAQL 540
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                                                                                                                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    951 ---KITDHVLKGTTSLANHTNELLGLGDESLCNLETTIEDTSLVKLETTGDTPSKRELPA 1007
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                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      801 LLKGSNPSSVSKEKIN 816
                                                                                                                                          COMPUTER: Hr you OPERATING SYSTEM: MSI
                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rockville
                                                 CLASSIFICATION: 435
                                                                                                       APPLICATION NUMBER: US/08/961,083
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                          Maryland
                                                                                                                                                                                                                                                                                                                                                                                                              9410 Key West Avenue
                                                                                                                                                                                                               E: Diskette, 3.50 inch, 1.4Mb storage
HP Vectra 486/33
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                                                                                                                                                                                           MSDOS version 6.2
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3.4%; Score 144; DB 4; Length 1040;
Best Local Similarity 19.2%; Pred. No. 0.024;
Matches 154; Conservative 111; Mismatches 284; Indels 252; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
668 LNGATVRDLDIKTVSADSKENVAALAKAANSANINNVAVEGKISGAKSVAGLVASATNTV 727
                                              734 PAEPEVPQVETEKVEAQLKEAEVLLAKVTDSSL-----KANATETLAGLRNNLTLQI 785
                                                                                                617 YTLASDM-----TADEVSLGDKQTSYLTGAFTGSLIGSDGTKSYAIYDLKKPLFDT 667
                                                                                                                                               688 YVEHPDERPHSNDGWGNASEHVLGKKDHS------EDPNKNFKADE--EPVEET 733
                                                                                                                                                                                              564 KVTVAVDQLVEEGTDGYK------DDYTFTVAKSKAEQPGVYTSFKQLVTAMQSNLSGV 616
                                                                                                                                                                                                                                             642 -VEVKNGNLIIPHKDHYHNIKFAWFDDHTY------KAPNGYT-LEDLFATIK-----Y 687
                                                                                                                                                                                                                                                                                              531 TDTAKYFVKVK-----TTENTDGTY 563
                                                                                                                                                                                                                                                                                                                                             586 KVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRLPYMVEHT---- 641
                                                                                                                                                                                                                                                                                                                                                                                            485 E--ENTETSTQDFQL--EYKKIETKDIDSVELYGKENDRY-----RRYL---SLSEAP 530
                                                                                                                                                                                                                                                                                                                                                                                                                                             526 SQIEYTEDEVRIAQLADKYTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKE 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 AYVS----AKTQVFHG-DKLVKEVDIENPAKEQVISG-LDYYTPYTVKTHLTYNLGENN 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470 AHKALFENKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPI---TH-PERLGKPN 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 KEVSRTEVA---PVNEVVKVGTLVKVKPTVEITNLTKVEN----KKSITVSYNLIDTTS 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 KGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLL--TE 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 PALEVTTRNRTEIQNIPYTTEEIQDPTLLKNRRKIERQGQAGTRTIQYEDYIVNGNVVET 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       379 PGPQPA-----KIDSNSSLVSQLVR---KVGEGYVFEE 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1040 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 LATKGTQEPGHE-----GKATVREETLEYTEPVATKGT-----QEPEHEGERXVEEEL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 RTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPTPEPS 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 PEYKLPLETKGTQEPGHEGEAAVREDLPVYTKPLETKGTQGPGHEGEAAVREEEPAYTEP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 KVSL---QGEASGDDG------ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 IKVDGKYYV-YLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRND-------G 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 QLYKLPLSQRHVESDG------LVF-----LVF-----DPAQITS 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 S------QVEQNPDHKGESVVRPTVPEQGNPVSATTVQSAEEEVLATTND-----R 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 SGRGNLSNSRTYRRQNSDNTSRTNWVPSYSNPGTTNTNTSNNSNTNSQASQSNDIDSLLK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 AVALARSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 LKIEGYQYIGYIK-TKKQDNTELSRTVDGKYSAQRDSQPNSTKTSDVVHSADLEWNQGQG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/976,255
FILING DATE: No. 6136581ember 21, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,675
FILING DATE: No. 6136581ember 22, 1996
ATTORNEY/ACENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08976255 Patent No. 6136581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1503 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION: (213) 489-1600
718 ELSENFLFLQEKNLLKGSLSSKEHINDLQT-----ELKNAGFTEAMLETSCRNSLDTEL 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
MEDIUM TYPE: MEDIUM TYPE: STORAGE
MEDIUM TYPE: MEDIUM 
                                                                       224 ELAAAEAFLSGRGNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTT----NTNTSNNSNTNS 279
                                                                                                                                                           687 KEKPRK-----DPLNVQ 717
                                                                                                                                                                                                                                                                                                                   637 ----NDVDKSEDLPSHQKIFDLMELNG-VQADFKPATLSSSLD-----NPKESVITGHFE 686
                                                                                                                                                                                                                                                                                                                                                                                               105 MKDPNYKLKDEDIVNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHSQHRE 164
                                                                                                                                                                                                                                   165 GGTPRNDGAVALARSQGRYTTDDGYIFNASDI-IEDTGDAYIVPHGDHYHYIPKNELSAS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           582 TGPELSQLTALRSVELEESSTDEDFFQSSTDPKDSSLPGDLHVTSGPESPFNNIF----- 636
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APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 TPDEVSKREGINAEQIVIKITDQGYVTSHGD------HYHYYNG-KVPYDAIISEELL 104
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: FastSEC
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67-3510
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633 West Fifth Street
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Patent No. 5739026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1004 ---- DVHEALLDSLGSH-TP------ QKLVPPDKPADSGYETENLESPEWTLHPAP 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1128 LVLVQEQPLPEPVLPEQSPAAQDSCLEARKSQPDESCLSALHNSSDLELRAT 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1090 -----SETFTAGSQGSYRD-----SAYFSDNDSEPEKR-----SEEVPG-----TSPSA 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 FIPYSOMSELEERIARIIPLRYRSNHWVPDSRPEQPSPQPT-----PEP-----SPGP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 QASQSNDIDSLLKQLYKLPLSQRHVESDG-----LVFDPAQITSRTARGVAVPHGDHYH 333
                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Garoff, Henrik APPLICANT: Liljestrom, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604 DADVKANP--TGDSAAAIYNRVKGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHNIK 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         963 GLVSALSSDSTSQDSLLEDSLSAPFPASEPS-LETPDS-LESV------ 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 -SHTLTAKKENVAPR----DQEFYDKAYNLLTEAHKALFENKGRNSDFQALDK----- 489
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SEQUENCE CHARACTERISTICS:
                                                                                             REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA Expression Systems Based on TITLE OF INVENTION: Alphaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662 FAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDERPHSNDGWGNASEHVLGKKDHSEDPNK 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Box 747
CITY: Falls Church
STATE: Virainia
                                                                                                                                                        NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 13-AUG
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                      TELEFAX:
                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                              Sequence 2, Application US/08466277 Patent No. 6190666 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1523 KGYSTTDGSLYSYFEGTKFNQAAIDMAEILTLWPRLQEANEQICLYALGETM------ 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1575 ------DNIRSKCPVN------DSDSSTPPRT-VPCLCR------YAMTAE 1606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1971 ---GSDSCLDRATFCPAKLRCYPKHHAYHQPTVRSAVPSPFQNTLQNVLAAATKRNCNVT 2027
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      2086 FAKTHNLVPLQEVP-MDRFTVDMKRDVKVTPGTKH 2119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 ISR---YVFAKDLPSETVKNLESKLSKQESVSHTLTAKKENVAPRDQEFYDKAYNLLTEA 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519 ERLGKPNSQIEYTEDEVRIA----QLADKYTTSDGY-IFDEHDIISDEGDAYVTPHMGHS 573
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                                                                                                                           TITLE OF INVENTION: DNA Expression Systems Based on
                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  APPLICANT: Garoff, Henrik
                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----IPLVRLPYMVEHTVEVKNGNLIIPHKDH 656
ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: P.O. Box 747
                                                                                                                                                                Liljestrom, Peter
                                                                                                             Alphaviruses
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1921 RPVYSPTVIERESSPDVAIAACNEYLSRNYPTVASYQITDEYDAYLDMVD----- 1970
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                         1862 EKLLLKMQMHPSEANKSRYQS-RKVENMKATVVDRLTSGARLYTGADVGRIPTYAVRYP 1920
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                                                519 ERLGKPNSQIEYTEDEVRIA----QLADKYTTSDGY-IFDEHDIISDEGDAYVTPHMGHS 573
                                                                                                                                                             471 HKALF-----ENKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAP---ITHP 518
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                                                                                                                                                                                                                                                                                                                                                                           359 HWVPDSRPEQPSPQPTPEPSPGPQPAPNLKI-----DSNSSLVSQLVRKVGEGYVFEEKG 413
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LENGTH: 2431 amino acids
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TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM_PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828-103P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/466,277
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
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19.7%; Pred. No. 0.18;
ative 93; Mismatches 253; Indels 212; Gaps
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Query Match 3.2%; Score 135.5; DB 1; Length 740; Best Local Similarity 17.7%; Pred. No. 0.061; Matches 145; Conservative 109; Mismatches 262; Indels 305; Gaps

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US-08-257-073-5
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                                                                                                                          TELEX: 425066 CURTMS INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
              MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 1
FILING DATE: 18-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,783
FILING DATE: 11-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/257,073
                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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APPLICANT: de Taisne, Ch
APPLICANT: Tine, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2086 FAKTHNLVPLQEVP-MDRFTVDMKRDVKVTPGTKH 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2028 QMRELPTMDS--AVFNVECFKRYACSGEYWEEYAKQPIRITTENITTYVTKLKGPKAAAL 2085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1971 ---GSDSCLDRATFCPAKLRCYPKHHAYHQPTVRSAVPSPFQNTLQNVLAAATKRNCNVT 2027
                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            629 -----IPLVRLPYMVEHTVEVKNGNLIIPHKDH 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611 -----PTGDSAAAIYN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574 HWIGKDSLSDKE---KVAAQAYTKEKGI------LPPSP-----DADVKAN---- 610
                                                      TOPOLOGY:
                                                                                          TYPE:
                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 45
                                                                                                                                                                                                                                                          NAME: Frommer, William S. REGISTRATION NUMBER: 25,5
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 20-MAI
                                                                                                            LENGTH:
                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
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                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                      740 amino acids
                                                                                                                                                                                  (212) 840-3333
(212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Curtis, Morris & Safford, p.C. 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paoletti, Enzo
de Taisne, Charles
              peptide
internal
                                                                                                                                                                                                                                                                                                                      20-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                            18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALARIA RECOMBINANT POXVIRUS VACCINE
                                                                                                                                                                                                                                                                                                                                                                                            US 07/852,305
                                                                                                                                                                                                                                                                                                                                      US 07/672,183
                                                                                                                                                                                                                                          454310-2570
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RESULT 11
US-08-447-031A-2
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                                                     APPLICANT: SWITALSKI, Lech
TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL
TITLE OF INVENTION: ITS PREPARATION
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                       APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 RSQGRYTTDDGYIFNASDIIEDTGDAYIVPHGDHYHYIPKNELSASELAAAEAFLSGRGN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 VNEVKGGYVIKVDGKYYVYLKDAAHADNVRTKEEINRQKQEHSQHREGGTPRNDGAVALA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 ----TNEEYVEEL------KKGILDMGIKLLFSK--VKSLLKKLKNKIFPKKKE 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 DHYHFI----PYSQMSELEERIARIIPLRYRSNHWVFDSRPEQPSPQPTPEPSPGPQPAP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 LNQGKEIGENLLNITKMNLGDKNNLESFPLDQLNMLKDNLI----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 LKQ------LYKLPLSQRHVESDGLVFDPAQITSRTARGVAVPHG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 ------VNDVLNVNMKNMITGNNFMDVVKSTLAQSGGLGSNDLINF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 LSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNN-----SNTNSQAS--QSNDIDSL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262
                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      519 PPTQSKKKNKNETVSGMDENFDN------HPENYFKEEYYYDENDDMEVKVKKI--- 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 QALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYTED-EVRIAQLADK 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 NLKIDSNSSLVSQLVRKVGEGYVFEEKGI----SRYVFAKDLPSETVKNLESKLSKQESV 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 R---EGINAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 IKFAWFDDHTYKAPNGYTLEDLFATIKYYVEHPDER-----PHSNDGWGNASEHVLGKKD 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         715 HSEDPNKNEKADEEPVEETPAEPEVPQVETEKVEAQLKEAE 755
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TNDE-----EDTND-----EEDH----ENNNATAYELGIVP------ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KATYSFVNTKKKIISLKSQGHKKETSQNQNENNDNQKYQ-----EVNDEDD 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DADVKANPTGDSAAAIYNRV----KGEKRIPLVRLPYMVEHTVEVKNGNLIIPHKDHYHN 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTTSDGYIFDEHDIISDEGDAYVTPHMGHSHWIGKDSLSDKEKVAAQAYTKEKGILPPSP 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHTLTAKKENVAPR-------DQEFYDKAYNLLTEA---HKALFENKGRNSDF 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GVTLKKFEPLKN-GNVSETIKLIH------LGNKDKKHIEAINNDIQIIK--- 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNQAVDTKSMEEPKVKAQPALRGVEPTEDSNIMNSINNVMDEIDFFEKELIENNNTPNVV 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NYEFILNNLKTSVLNKLKDLLLRLLYKAYVS--YKKRKAQEKGLPEPTV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QELQAIYNELMNYTNGNKNIQQIFQQNILENDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKEKEEKEKEKEKEKEKEKEKEEKEEEKKEKEEEQEE 724
                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                       GUSS, Bengt
HOOK, Magnus
JONSSON, Hans
LINDBERG, Martin
                                                                                                                                                              PATTI, Joseph
SIGNAS, Christer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LNQETEEEMEKQVEAITKQIEAEVDALAPK-----NKEEEEKEKEK 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DEEDTNDDEDTNDEEDTNDDEDTNDDED-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.2%; Score 135.5; D
Best Local Similarity 19.2%; Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703) 836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 07/861,804
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9003374-7
FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCGOWAN, MAlcolm K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: V
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 22-MA CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 KDAAHADNVRTKEEINROKQEHSQHREGGTPRNDGAV------ALARSQGR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 NNEKSYV-SKDITIK-----DQIQGGQQLDLSTLNINVT------GTHSNYYSGQ-- 237
                                                                                                                                                                                                                                                       404
                                                                                                                                                                                                                                                                                                                                              353 LSKKDGSVVKDNQKEIEIITDANGIANIKALPSGD---YILK-----EIEAPRPYTFDK 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                295 SQAWYQEH--GKEEVNGKSFNHTVHNINANAGIEGTVKGELKVLKQDKDTKAPIANVKFK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
406 GYVFEEKGISRYVFAKDLPSETVKNLESKL------SKQESVSHTLTAKKENVAPRD 456
                                                                                                 354 RYRSNHWVPDSRPEQPSPQPTPEPSPGPQPAPNLKIDSNSSLVSQLVRKVG-----E 405
                                                                                                                                                                                                 296 KLPLSQRHVESDGLVFDPAQITSRTARGVAVPHGDHYHFIPY--SQMSELEERIARIIPL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 NNRVSYIDGKQATQKTENLTPDEVSKREGINAEQIVIKITDQGYVTSHGDHYHYYNGKVP 94
                                                        484 -----W--SNLPEN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDAIISEELLMKDPNYKLKDEDIVNEVK-----GGY-----VIKVDGKYYVYL 137
                                                                                                                                                                                                                                                 ---DKEYPFTMKDTDNQGYF------ 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SAITDFEKAF--PGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNN 294
                                                                                                                                                                                                                                                                                                GNLSNSRTYRRQNSDNTSRTNWVPSVSNPGTTNTNTSNNSNTNSQASQSNDIDSLLKQLY 295
                                                                                                                                                                                                                                                                                                                                                                                                  YTTDDGYIFNAS----DIIED-TGDAYI--VPHGDHYHYIPKNELSASELAAAEAFLSGR 235
                                                                                                                                                     ------VWEGTQKVKPTIYFKLYKQDDNQNTTPVDKAEIKKLEDGTTKVT-- 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1183 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 120; Mismatches 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                           ---DKNGKAIKYLVKEVNAQGEDTTPE 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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US-08-015-973-1
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INFORMATION FOR SEQ ID NO: 1:
    REFERENCE/DOCKET NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)89-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SON "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Schles:
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,973
FILING DATE: 10-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            962 KYDEGKKIEYTVTEDH-----YKDYTTDINGTTITNKYTPGETSATVTKNWD-----DNNN 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   902 NKYTPETTSISGEKVWDDKDNQDGKRPEKVSVNLLANGEKVKTLDVTSETNWKYEFKDLP
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                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          743 KYSVNLLADGEKVKTLDVTSE-----TNWKYEFKDLPKYD------EGKKIEYTVTE 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581 -----LSDKEKVAAQAYTKEKGILPPSPDADVKANPTGDSAAAIYNRVKGEKRIPLVRL 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         692 EL-----TKVKGYTTHVDNNDMGNLIVTNKYTPETTSISGEKVWDDKDNQDGKRPE 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 EVRIAQLADKYTTSDGYI--FDEHD----IISDEGDAYVTPHMGHSHWIGKDS----- 580
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                                                                                                                                                    Misrock, S. Leslie
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 169;
1711 L-HASSGFTEEFEEVQSCTVDLGITADSSNHPDNKHKN 1747
                                                                                                                                                                                   1597 PTSSVTSENSEVFHVSEAEASNSSHESRIGLAEGLESEKKAVIPLVIVSALTFICLVVLV 1656
                                                                                         1657 GILIYWRKCFQTAHF-----YLEDSTSPRVISTPPTPIFPISDDVGAIPIKHFPKHVAD 1710
                                                                                                                                                                                                                                                                                     1537 SKAWAVLTSDEESGSGQGTSDSLNENETSTDFSFADTNEKDADGILAAGDSEITPGFPQS 1596
                                                                                                                                                                                                                                                                                                                                                                                  1479 ENSEEDNRVTSVSSDSQTGMDRSPGKSPSANGLSQKHNDGK--EENDIQTGSALLPLSPE 1536
                                              695 RPHSNDGWGNASEHV-----LG----KKDHSEDPNKN 722
                                                                                                                                        647 GNLIIPHK----DHYHNIKFAWFDDHTY------KAPNGYTLEDLFA-TIKYYVEHPDE 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1426 DDDDDDRGSDGLSIHKCMS-CSSYRESQEKVMND-----SDTHENSLMDQNNPISYSLS 1478
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                                                                                                                                                                                                                                    603 PDADV-----KANPTGDSAAAIYNRVKGEKR--IPLVRLPYMVEHTVEVKN 646
                                                                                                                                                                                                                                                                                                                                   562 GDAYVTPHMGHSHWIGK---DSLSDKEKVA--AQAYTKEK---GIL------PPS 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 DGLVFDPAQ------ITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRY 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             994 GEW-----SGASSDS------ 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: A NOVEL RECEPTOR TITLE OF INVENTION: PHOSPHATASE-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-FEB-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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LENGTH: 2308 amino aci
1205 DPILVETPKVDKISSTMLHLIVSNSASSENMLHSTSVPVFDVSPTSHMHSASLQGLTISY 1264
                                                                         1091 SISSTKGMFPGSLAHTTTKVFDHEISQVPENNFSVQPTHTVSQASGDTSLKPVLSANSEP 1150
                                                                                                                                                                                                                       1031 TSVFGDDNKALSKSEIIYGNETELQIPSFNEMVYPSESTVMPNMYDNVNKLNASLQETSV 1090
                                                                                                                                                                                                                                                                                                                                 131 GKYYVYLKDAAHADNVRTKEEINROKQEHSQHREGGTPRNDGAVAL-----ARSQGRYT 184
                                    307 DGLVFDPAQ-----ITSRTARGVAVPHGDHYHFIPYSQMSELEERIARIIPLRY 355
                                                                                                            260 SVSNPGTT-----NTNTSNNSNTNSQAS-QSNDIDSLLKQLYKLPLSQRHVES 306
                                                                                                                                                                                    230 AFLSGRG-----RTIWVP 259
                                                                                                                                                                                                                                                            185 T----DDGYIFNASDIIEDTGDAYIVPHGDHYHY-----IPK-----NELSASELAAAE 229
                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 18,872 REFERENCE/DOCKET NUMBER: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
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(212)869-8864/9741
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                                                                                                                                                                                                                                                                                                                          ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Margolis, Richard U.
TITLE OF INVENTION: A NEW CLASS OF RPTPases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        695 RPHSNDGWGNASEHV-----LG----KKDHSEDPNKN 722
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                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                   TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
                                                                                                                NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30742
                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/081,929
                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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1155 Avenue of the Americas
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Grumet, Martin H.
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3.2%; Score 135; DB 4; Length 2308;
Best Local Similarity 19.2%; Pred. No. 0.4;
Matches 169; Conservative 123; Mismatches 276; Indels 310; Gaps
1711 L-HASSGFTEEFEEVQSCTVDLGITADSSNHPDNKHKN 1747
                                                                        1657 GILIYWRKCFQTAHF-----YLEDSTSPRVISTPPTPIFPISDDVGAIPIKHFPKHVAD 1710
                                                                                                                                                  1597 PTSSVTSENSEVFHYSEAEASNSSHESRIGLAEGLESEKKAVIPLVIVSALTFICLVVLV 1656
                                                                                                                                                                                                                              1537 SKAWAVLTSDEESGSGOGTSDSLNENETSTDFSFADTNEKDADGILAAGDSEITPGFPQS 1596
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                                                                                                                                                                                                                                                                                                                                                                                           1426 DDDDDDRGSDGLSIHKCMS-CSSYRESQEKVMND-----SDTHENSLMDQNNPISYSLS 1478
                                        695 RPHSNDGWGNASEHV-----LG----KKDHSEDPNKN 722
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                                                                                                                                                                                                                                                                  562 GDAYVTPHMGHSHWIGK---DSLSDKEKVA--AQAYTKEK---GIL------PPS 602
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
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5268270-2
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**NEGATIVE HOST CELLS**
**NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Patent No. 5268270
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1200 GLQPRAAQPRTQAAAQADAVSTNTNSALSDAMASTQSILLDTG-AYLTRH-----IAQK 1252
                                                                                    1154 Q--FHSKSRNR--RAISS--EPSSDEDASESVSTSD-----KHPQDNTELHEKVETA 1199
                                                                                                                                                                       1094 RPPAPVFSLDDYDAKDNSESSIGNLARVPIRMGRELINDYEEIPLEELEDEAEEERRQAT 1153
                                                                                                                                                                                                                                                       1034 RKAAEIARQQEEARKAAELAAKQKAEAERKARELARQKAEEASHQANAKPKRRRRAILP 1093
                                           532 EDEVRIAQ------LADKYTTSDGYIFDE-----HDIISDEGDAYVTPHMGHSHWIGKD 579
                                                                                                                           472 KALFENKGRNSDFQALDKLLERLNDESTNKEKLVDDLLAFLAPITHPERLGKPNSQIEYT 531
                                                                                                                                                                                                                455 RD-----QEFYDKAYNLLTEAH 471
                                                                                                                                                                                                                                                                                                401 RKVGE-GYVFEEKGISRYVFAKDLPSETVKNLESKLSKQESVSHTLTAK-----KENVAP 454
                                                                                                                                                                                                                                                                                                                                            974 KATQTDGAQIAKPQNIVVAPPSPQANQAEELRQQAKAEQVKRQQAAEAEKVARQKDEEAK 1033
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           746 -- NGDEVCVRSDYTGYVTCNTGNLSDKALNSFDXATKINGNVNLNQNAALVLGKAALWGK 803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627 GHNGALNLNFNGKSAQNRFLLTGGANLNGK-ISVTQGNVLLSGRPTPHARDFVNKSSARK 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 RNDGAVAL----ARSOGRYTTDDGYIFNASDIIEDTGDAYI----VPHGDHY------ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                567 YALKSGGRLNAPMPENGVAENNDWIFMGYTQEEARKNAMNHKNNRRIGDEGGFFDEENGK 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 YVIKVDGKYYVYLKDAAHADN-----VRTKEEINROKQEHSQHR----EGG-----TP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 ITNPNSLSVHSIQNDYDEDDYSYYYRPRRPIPQ--GKDLYYKNYRY------ 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 ITDQGYVTSHG------DHYHYYNGKVPYDAIISEELLMKDPNYKLKDEDIVNEVKGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-JUL-1987
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